

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 15 and

TO: Catherine Joyce

Location: REM/4C04/3C18

Art Unit: 1642

Tuesday, October 04, 2005

Case Serial Number: 10/645094

From: Edward Hart

Location: Biotech-Chem Library

REM-1A55

Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Joyce,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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STIC-Biotech/ChemLib

167604

From:

Joyce, Catherine

Sent:

Monday, October 03, 2005 4:11 PM

To:

STIC-Biotech/ChemLib

Subject:

10/645094

Please search the following sequences:

SEQ ID NO:1 (polypeptide)

Catherine Joyce Art Unit 1642 Ph. 571-272-3321 Office: 4C04 Mailbox: 3C18

RECEIVED

OCT -4 20:

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search
NA# AA#:

S/L: Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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Protein Sèquence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file
 extension .rup) that can no longer be found in the database, the permanent record with the new
 accession number can be found by searching the old accession number in the UniProt Protein
 Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession

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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions rapm and rapm

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech:Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

Voluntary Results Feedback Form	VOIDTANIA ROSTILS SOOTIAGE ASTAT
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> I am an examiner in Workgroup:	Example: 1610
> Relevant prior art found, search results used a	as follows:
102 rejection	•
☐ 103 rejection	
Cited as being of interest.	
Helped examiner better understan	d the invention.
Helped examiner better understan	d the state of the art in their technology.
Types of relevant prior art found:	
☐ Foreign Patent(s)	
Non-Patent Literature (journal articles, conference proceeding)	gs, new product announcements etc.)
> Relevant prior art not found:	
Results verified the lack of relevant prior a	art (helped determine patentability).
•	tentability or understanding the invention.
Comments:	

Drop off or send completed forms to SIIC Biotech Chemil brany Remsen Bidg



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Thuman anisakisis.";

J. Immunol. 165:1491-1497(2000).

B. EMBL; AJ40081; CAC00499.1;

CO; GO: 0016491; F: Poxidoreductase activity; IEA.

GO; GO: 0016491; F: Poxidoreductase activity; IEA.

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R InterPro; IPR00019; Amineoxidase; I.

R PRINTS; PR00419; AMXEDTASE.

R PRINTS; PR00419; AMXEDTASE.

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Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei;
Acanthomorpha; Acanthopterygii, Percomorpha; Perciformes; Scombroidei;
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Yonehara S.;
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Endoplasmic reticulum lumenal L-amino acid oxidase precursor.
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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MELAUSEER R.D., Feingold E.A., Grouse L.H., Derge J.G.,

R. Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Joederg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Caraninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarante P.H.,

Richards S.W. Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

A Nichards S.W., Soung A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., McEwan S.D., McEwan S.D., Schnetch A., Schlet A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., McEwan S., Schlet S.D., Schnetch A., Schlet B.,

R. Jones S.J., McEwan B., Stalska D., Smailus D.E., Schnetch A., Schlet B.,

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                                                                                                                                                 TALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVS
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                                                                                  DLLDRALQKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMY
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                                                                                                                                                                                                                                                                                                                                                                                                                      FAGEHTAFPHAWIETSMKSAIRAATNINKVANEESTIEHTKDEL 524
                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017599; AAH17599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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MEDLINE=21240157; PubMed=11341935; DOI=10.1016/S0167-4838(00)00229-6;
Takatesuka H., Sakurai Y., Yoshioka A., Kokubo T., Usami Y., Suzuki M.,
Matsui T., Titani K., Yagi H., Matsumoto M., Pujimura Y.;
"Molecular characterization of L-amino acid oxidase from Agkistrodon
halys blomhoffii with special reference to platelet aggregation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIH---GEQVWDKCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 YLVNGVRERTYVVQENPDVLKYNVSESEKGI6ADDLLDRALQKVKEEVBANGCKAALEKY
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
M-LAO precursor (EC 1.4.3.2).
Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
Ekkaryota, Metzazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Gloydius.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      523;
                                                                                                                                                                                                                                                                                                                                                                                                                                             42.8%; Score 1156.5; DB 2; Length ilarity 47.1%; Pred. No. 3.6e-63; Conservative 85; Mismatches 172; Indels
HSSP; PB1362; Lacil.

(MD), MG12140628; Lacil.

(GO; GO:0005615; C:extracellular space; TAS.

(GO; GO:0001716; F:L-amino-acid oxidase activity; IDA.

(GO; GO:0001716; F:L-amino acid catabolism; IDA.

(GO; GO:0009063; P:amino oxidase; 1.

(Fam; PF01553; Amino oxidase; 1.

(R PRINTS; PR00419; ADXRDTASE.

(R PRINTS; PR00757; AMINEOXDASEF.

(PRINTS; PR00757; AMINEOXDASEF.

(PRINTS; PR00757; AMINEOXDASEF.

(PRINTS; PR00757; AMINEOXDASEF.

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Best Local Similarity
Matches 235; Conserv
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P8138; OSTB49;
15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
L'amino-acid oxidase precursor (EC 1.4.3.2) (LAO) (LAAO) (Apoxin I).
Agkistrodon rhodoscoma (Malayan pit viper) (Calloselasma rhodoscoma).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
N'Uperidae; Crocalinae; Calloselasma.
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MEDLINE-21145470; PubMed=11248687;
Macheroux P., Seth O., Bollschweiler C., Schwarz M., Kurfuerst Au L.-C., Ghisla S.;
"L.-amino-acid oxidase from Malayan pit viper Calloselasma
                                                                                                                                                                                                                                                                                                504;
                                                                                                                                                                                                                                                                                           ; Score 1089.5; DB 2; Length
; Pred. No. 4.7e-59;
97; Mismatches 167; Indels
     (OCT-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                              504 AA; 57124 MW; AEB034155184F0A7 CRC64;
                                                                             IEA
                      EMBL, AY450403; AAR20248.1;
PDB; 1REO; X-ray; A=-.
GO; GO:001716; F.L-amino-acid oxidase activity;
GO; GO:0016491; F:Coxidoreductase activity;
GO; GO:001818; P:electron transport; IEA.
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR00205; NAD BS.
Pfam; PF01593; Amino_oxidase; 1.
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                                                                                                                                                                                                                                                                                              40.3%;
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Best Local Similarity 44.0%
Matches 213; Conservative
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
L-amino acid oxidase (EC 1.4.3.2).
Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys pallas).
Elemaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi, Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae, Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                           504;
                                                                                                                                                                                                                                                                                                                                        40.6%; Score 1096.5; DB 2; Length 44.4%; Pred. No. 1.7e-59;
                                                                                                                                                                                                                                                                                                                                                                                        166; Indels
                                                                                                                                                                                                                                                                     Potential.
17F57B46E646F12A CRC64;
                                                                                       PDB; 1TDO; X-ray; A=-.
GO; GO:0001716; F:L-amino-acid oxidase activity
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO:00006118; F:ealectron transport; IEA.
Pfam; PF01593; Amino_oxidase; 1.
PRINTS; PR00757; AMINEOXDASEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 AA
                                                                                                                                                                                                                                                                                                                                                                                        96; Mismatches
Biochim. Biophys. Acta 1544:267-277(2001)
EMBL; ABO73192; BAB69450.1; -.
PDB; ITDK; X-ray; A=-.
PDB; ITDN; X-ray; A=-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom gland;
Zhang H., Zhang T., Teng M., Niu L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 215; Conserv
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Q6STF1
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39.9%; Score 1079.5;
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                                                                                                                                                              Vrielink A.;

"The structure of L-amino acid oxidase reveals the substrate trajectory into an enantiomerically conserved active site.";

EMBO J. 19:4204-4215(2000).

EMBO J. 19:4204-4215(2000).

C. !- FUNCTION: Catalyzes an oxidative deamination of predominantly hydrophobic and aromatic L-amino acids. Has an antibacterial effect and an ability to induce apoptosis. The H(2)O(2) produced by L-amino acid oxidation is involved in the apoxin-I induced apoptosis and hemorrhage caused by the venom.

C. I. CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid + H(3) + H(2)O(2).

C. I. COFACTOR: FAD.

C. I. SUBUNIT: Homodimer.

C. I. SINILARITY: Belongs to the flavin monoamine oxidase family.

Strong, to mammalian FIGI.
                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                  TISSUE=Venom;
MEDLINE=94361525; PubMed=8080286; DOI=10.1006/abbi.1994.1401;
MEDLINE=94361525; PubMed=8080286; DOI=10.1006/abbi.1994.1401;
Ponnudurai d., Chung M.C.M., Tan N.-H.;
Purification and properties of the L-amino acid oxidase from Malayan pit viper (Calloselasma rhodostoma) venom.";
Arch. Biochem. Biophys. 313:373-378(1994).
                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND CARBOHYDRATE-LINKAGE SITES
                                                                                                                                    TISSUE=Venom;
MEDLINE=20402326; PubMed=10944103; DOI=10.1093/emboj/19.16.4204;
Pawelek P.D., Cheah J., Coulombe R., Macheroux P., Ghisla S.,
 rhodostoma:comparative seguence analysis and characterization of active and inactive forms of the enzyme.";
Eur. J. Biochem. 268:1679-1686(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ271725; CAB71136.1; ---
R BMB; IFR8; X-ray; A/B/C/D=19-516.
R GlycosuiteDB; PB1382; ---
R InterPro; IPR000759; Adrndx reductase.
R InterPro; IPR001613; Amineoxid £1.
R InterPro; IPR002937; Amino oxidase.
R InterPro; IPR002597; Amino oxidase.
R PRINTS; PR00419; ADXRDTASE.
R RRINTS; RR00419; ADXRDTASE.
R R RINTS; RR00419; ADXRDTASE.
R AD-structure; Direct protein sequencing; FAD; Flavoprotein; SIGNAL
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N-linked (GlCNAc. .).
N-linked (GlCNAc. .).
C -> E (in Ref. 2).
D -> N (in Ref. 2).
                                         SEQUENCE OF 19-38 FROM N.A.
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DB 1; Length 516; 58221 MW; 5F9435718B3A3BDE CRC64;

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RVGGRVETYRNEKEGWYAEMGAMRIPSSHRIVQWFVKKLGVEMNEFVMTDDNTFYLVNGV 152
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                                                                                                                                                                                                                                                                                                 FLSVL--DVPILLNSKVKHIRQSDKGVIVSYQT-GNESSLMDLSADIVLVTTTAKAALFI 329
                                                                                                                                                                                                                                                                                                                                                            DPDPPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIRGGKSITDGPSRYIYYPSHSF 389
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                                                                           LEECFRETDYEBFLEIAKNGLTATSNPKRVVIVGAGMAGLSAAYVLAGAGHQVTVLEASE
                                                LADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTILEAND
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
              Mismatches 169;
   Pred. No. 2e-57
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Bothrops jararacussu (Jararacussu).
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                 96
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498 VNRASENPSGIHLSND 513
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45.1%;
44.08;
                218; Conservative
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   Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                     RERTYVVQENPDVLKYNVSESEKGISADDLLDRALQKVKEEVEANGCKAALEKYDRYSVK 212
                                                                                                                                                                                                                                  EYLKBEGGLSPGAVRMIGDLINEQSLMYTALSEMIYDQADVNDSVTYHBVTGGSDLLPEA 272
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                                             LADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTILEAND
                                                                 Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
FAD-Containing L-amino acid oxidase Apoxin 1.
Crotalus atrox (Western diamondback rattlesnake).
Exharyotas, Metazota, Chordata, Craniata; Vertebrata, Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Crotalinae; Crotalinae;
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Toril S., Mashima T., Naito M., Haga N., Yamane K., Yamamoto Fox J.W., Turuo T.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                 Indels
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Pred. No. 2e-58;
92; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR00759; Adrndx reductase.
InterPro; IPR002937; Adino_cxidase.
InterPro; IPR002037; Adino_cxidase.
InterPro; IPR00103; PyrIdine_redox_2.
Pfam; PP01593; Amino_cxidase; 1.
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PRINTS; PR00469; PNDRDTASEII.
44.48;
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HSSP; P81382; 1F8R.
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                219; Conservative
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 Best Local Similarity
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NCBI_TaxID=8730;
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              Matches
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RESULT 6 69PWC9

SO DE REPERENTATION OF THE PROPERTY OF THE PRO

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SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                               213 EYLKEEGGLSPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVTGGSDLLPEA 272
                                                                                                                                                                                                                                                                                                                    273 FLSVLDVPILLINSKVKHIRQSDKGVIVSYQTGNESSLMDLSADIVLVTTTAKAALFIDFD 332
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                                                                                                                                                                                                                                                                                                                                                                                                                           319 PPLPPKKAHALRSVHYRSGTKIFLTCTKKFWEDDGIHGGKSTTDLPSRFIYYPNHNFPNG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||::|| | |:::|| 379 --VGVIIA-YGIGDDANYFEALDFEDCGDIVINDLSLIHQLPKEEIQAICRPSMIQRWSL 435
                                                                      79
                                                                                                                             80 RAGGQVKTYRNEKEGWYANLGPMRLPEKHRIVREYIRKFGLQLNEFSQENENAWYFIKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raibekas A.A., Massey V.,
"Primary structure of the snake venom L-amino acid oxidase shows high homology with the mouse B cell interleukin 4-induced Figl protein."; Biochem. Biophys. Res. Commun. 248.476-498 [1998].
-!- FUNCTION: Catalyzes an oxidative deamination of predominantly hydrophobic and aromatic L-amino acids. Has an antibacterial effect and an ability to induce apoptosis. The H(2)0(2) produced by L-amino acid oxidation is involved in the apoxin-1 induced apoptosis and hemorrhage caused by the venom.
-!- CATALYTIC ACTIVITY: An L-amino acid + H(2)0 + O(2) = a 2-oxo acid + NH(3) + H(2)0(2).
                                                         EYLLKEGNLSPGAVDMIGDLLNEDSGYYVSFIESLKHDDIFAYEKRFDEIVGGMDKLPTS
                                                                                                                                                                                                                                                                                                                                            LADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTILEAND
                                                                                                       RVGGRVETYRNEKEGWYAEMGAMRIPSSHRIVQWFVKKLGVEMNEFVMTDDNTFYLVNGV
                                                                                                                                                                             RERTYVVQENPDVLKYNVSESEKGISADDLLDRALQKVKEEVEANGCKAALEKYDRYSVK
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 Gaps
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15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Crotalus adamanteus (Eastern diamondback rattlesnake)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the flavin monoamine oxidase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Venom;
MEDLINE=98369573; PubMed=9703950; DOI=10.1006/bbrc.1998.9024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPYSLGAFALFTPYOHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATABĀSE: NAME-Worthington enzyme manual;
WWW="http://www.worthington-biochem.com/LAO/".
 Mismatches 166;
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85;
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NCBI_TaxID=8729;
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 Conservative
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OXLA_CROAD
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 KFEPPLPPKKAHALRSVHYRSGTKIFLTCTKKFWEDDGIHGGKSTTDLPSRFIYYPNHNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 WSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMKSAIRAATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 WSLDKYAMGGITTFTPYOFOHFSEALTAPFKRIYFAGEYTAOFHGWIDSTIKSGLTAARD
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                     protein sequencing; FAD; Flavoprotein;
 restrictions
                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 516;
                                                                                                                                                                                                                                                                                                                                                                                  94; Mismatches 171; Indels
                                                                                                                                                                                                                                                                              19 516 L-amino-acid oxidase.

52 106 FRD (ADP part) (Potential)

379 N-linked (GLONG. ) (Po

516 AA, 58662 MW, FDFAA77A49FDA05A CRC64;
 There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 3.5e-57
                                                                                                                                                                                                                                                                                                                                                      39.2%; Score 1059.5;
                                                                                                               HSSP, P81382; 1F8R.
InterPro; IRR002937; Adrndx_reductase.
InterPro; IRR002937; Amino_oxidase.
InterPro; IRR002037; And BS.
InterPro; IRR000103; PyrIdine_redox_2.
Pfam; PF0153; Amino_oxidase; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00469; PNDRDTASEII.
Antibiotic; Apoptosis; Direct protein seglycoprotein; Oxidoxeductase; Signal; To
 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-amino acid oxidase (Fragment).
                                                                                  EMBL; AF071564; AAC32267.1; -. PIR; JE0266; JE0266.
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Q6TGQ8;
05-JUL-2004 (
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05-JUL-2004
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CARBOHYD
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Conservative 104;
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(TrEMBLrel. 25, I
(TrEMBLrel. 26, I
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Name=LAAO;
                                                                                                                                                                                                                                                                                                      Local Similarity
les 212; Conserv
                NCBI_TaxID=39682;
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01-MAR-2004
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                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 MYQAIQEKVHLNARVIKIQQDVKEVTVTYQT-SEKETLSVTADYVIVCTTSRAARRIKFE 311
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                                                                                                                                                                                                                                                                                                                                                                                  33 LADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTILEAND 92
                                                                                                                                                                                                                                                                                                                                                                                                 Pereira J.O.,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
L-amino acid oxidase.
Trimeresurus stejnegeri (Chinese green tree viper).
Trimeresurus stejnegeri (Chinese green tree viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosuria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 DPYSLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMK 498
Bothrops moojeni (Lance-headed viper) (Caissaca).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleost.
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea,
Viperidae; Crotalinae; Bothrops.
                                                                                       SEQUENCE FROM N.A.

A SOATES A.M., Kashima S., Roberto P.G., Astolfi-Filho S., Perri Giglio J.R., Franca S.C.;
L Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
L Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; A7398692; AAR31183.1; -.
R EMBL; A7398692; AAR31183.1; -.
R GO; GO:00064187; F:monooxygenase activity; IEA.
R GO; GO:0006118; P:electron transport; IEA.
R InterPro; IPR001619; Adradx_reductase.
R InterPro; IPR000960; Flav.cont_mnoxgn.
R InterPro; IPR000966; Flav.cont_mnoxgn.
R InterPro; IPR000966; Flav.cont_mnoxgn.
R PRINTS; PR00119; ADXRDTASE.
R PRINTS; PR00770; FWOXYGENASE.
                                                                                                                                                                                                                                                                                                                             39.2%; Score 1058.5; DB 2; Length
45.0%; Pred. No. 3.6e-57;
.ive 86; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                      555C159B029FB9CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 AA
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                                                                                                                                                                                                                                                                                                     54436 MW;
                                                                                                                                                                                                                                                                                                                              Query Match 39.2% Best Local Similarity 45.0% Matches 211; Conservative
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NON TER
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RVGGRVETYRNEKEGWYAEMGAMRIPSSHRİVQWFVKKLGVEMNEFVMTDDNTFYLVNGV 152
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                                                                                         "Molecular characterization of Trimeresurus stejnegeri venom L-amino
MEDLINE=22843468; PubMed=12963032; DOI=10.1016/j.bbrc.2003.08.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trimeresurus stejnegeri (Chinese green tree viper).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 516;
                      Zhang Y.J., Wang J.H., Lee W.H., Wang Q., Liu H., Zheng Y.T., Zhang Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                            acid oxidate with potential anti-HIV activity.";
Biochem. Biophys. Res. Commun. 309:598-604(2003).
BMBL; AN277739; AAG$6232.1; -.
GO; GO:0004497; F:monoxygenese activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001513; Amineoxid fl.
InterPro; IPR001950; Pav Cont_mnoxgn.
InterPro; IPR000205; NaD BS.
Pfam; PF01593; Amineoxid fl.
InterPro; IPR000205; NaD BS.
Pfam; PF01593; Amineoxid fl.
PRINTS; PR00177; AMINEOXDASEF.
PRINTS; PR00177; AMINEOXDASEF.
PRINTS; PR00177; AMINEOXDASEF.
SEQUENCE 516 AA; 58601 MM; FB5ACOBCI71B9288 CRC
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Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
L-amino acid oxidase precursor.
Name=Laol; Synonyms=mLAO;
Name=Laol; Synonyms=mLAO;
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musc.
                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                          38.9%; Score 1052.5; DB 2; Length 516; 42.7%; Pred. No. 9.4e-57;
  a; Squamata; Scleroglossa; Serpentes; Colubroidea;
Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative 103; Mismatches 171; Indels
                                                                                                Wang J., Huang Q., Teng M., Niu L.,
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, X138966, AAQ16182.1;
HSSP, P81382, 1FRR.
GO, GO:0016491, F.oxidoreductase activity, IEA.
GO, GO:0016491, F.oxidoreductase activity, IEA.
HINE-PFO: IPRE002937, Amino oxidase.
InterPro; IFRE002937, Amino oxidase.
InterPro; IFRE002059, NAD BS.
Pfam; PF01593; Amino oxidase; 1.
SEQUENCE 516 AA; 58644 WW; 2E52BD69Al3DBAE2 CRC64;
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STRAIN=ICR; TISSUE=Mammary gland;
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  Lepidosauria; Squamata;
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Matches 211; Conserv
                                                                               SEQUENCE FROM N.A.
                                         NCBI_TaxID=39682;
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87 ILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSHRIVQWFVKKLGVEMNEFVMTDDNTF 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 LSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 YLVNGVRERTYVVQENPDVLKYNVSESEKGIGADDLLDRALQKVKEEVEANGCKAALEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 DSYSTKAYLMKEGTLSKRAHR------DDRGYNDENAGYYKSLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                          Characterization and expression of L-amino acid oxidase of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49;
MEDLINE=22014058; PubMed=11907037; DOI=10.1074/jbc.M200936200;
Sun Y., Nonobe E., Kobayashi Y., Kuraishi T., Aoki F., Yamamot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.8%; Score 1048.5; DB 2; Length 43.5%; Pred. No. 1.7e-56; Lindels ive 79; Mismatches 166; Indels
                                                                                                                                       EMBL; AB03401; BAA97677.1; -. MISSP; BB1302, 1FRR.
MISSP; BB1302, 1FRR.
MGD; MGI:2140628; Laol.
GO; GO:000515; C:extracellular space; TAS.
GO; GO:000716; F:L-amino-acid oxidase activity; IDA.
GO; GO:0009063; F:amino acid catabolism; IDA.
InterPro; IPR000759; Adridx reductase.
InterPro; IPR000759; Amino-oxid fl.
InterPro; IPR000597; Amino-oxid fl.
InterPro; IPR000505; Mab BS.
InterPro; IPR000505; Mab BS.
InterPro; IPR000505; Mab BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
Potential.
8C5A4FE833BA4BC1 CRC64;
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FIG1 MOUSE

ID FIG1 MOUSE STANDARD; PRT; 630 AA. AC 009046; Q9CXK7;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
                                                                                                                        277:19080-19086(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01593; Amino oxidase; 1.
PRINTS; PR00419; ADKEDTASE.
PRINTS; PR00757; AMINEOXDASEF.
PRINTS; PR00370; PMOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58587 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523
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EMBL; AK014297; BAB29253.1; ALT_INIT.
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RESTRAIN=CSTBL/64); TISSUE=Embryonic head;

RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA MIKAIGO I., OBATON N., SAITOR N., SUZUKI H., YAMADAKA I., KIYOBAWA H.,

RA MIKAIGO I., OBATON N., SAITOR N., SUZUKI H., YAMADAKA I., KIYOBAWA H.,

RA MIKAIGO I., OBATON N., BUIT C., Hume D.A., QUECKENDEN J.,

RA BAIdarelli R., Hill D.P., BUIT C., Hume D.A., QUECKENDEN J.,

RA BAIAKE J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Kedzierski R.M., King B.L.,

RA MAGIOLT D.R., MAICAIN I.V., Lee Y., Lenhard B., Lyons P.A.,

RA MAGIOLT D.R., MAICAIN I.V., Lee Y., Lenhard B., Lyons P.A.,

RA MAGIOLT D.R., MAICAIS L., MATCHIONNI L., MCKENZIE L., Miki H.,

RA PETROVSKY N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Asvasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou W., Satou M.,

RA Verardo R., Wanner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Milming L.G., Wynehaw-Boris A., Yanagisawa M., Yang I., Yang I.,

Miyazaki A., Hashizume W., Imctani K., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Imctani K., Ishii Y., Itoh M., Kagawa I.,

RA Mayasaki A., Sasaki K., Sasaki D., Shibata K., Shinada A.,

RA Hara A., Hashizaki Y.,

RA Mayasaki A., Sasaki D., Saibata K., Shinagawa A.,

RA Hara A., Hashizaki Y.,

RA Hara A., Hashizaki Y.,

RA Hara A., Hashizaki Y.,

RA Mayasaki A., Sasaki D., Shibata K., Shinagawa A.,

RA Manayasa of the mouse transcriptome based on functional annotation of Rull Langth Collection?

C. I. CONTON PAN PAN PANDALLIAN.
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                                                                                                                                                                                                                                                                                                                                                                      "Expressed genes in interleukin-4 treated B cells identified by cDNA
                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c; TISSUE=Spleen;
MEDLINE=99012997; Pubmed=9798653; DOI=10.1016/S0161-5890(98)00031-5;
                                                                                                                                                                                                 Chu C.C., Paul W.E.;
"Fig1, an interleukin 4-induced mouse B cell gene isolated by CDNA representational difference analysis.";
Proc. Natl. Acad. Sci. U.S.A. 94:2507-2512(1997).
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-4 induced protein 1 precursor (Fig-1 protein) (mFIG1)
Name=11411; Synonyms=Fig1;
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDUCTION: By interleukin-4. SIMILARITY: Belongs to the flavin monoamine oxidase family. Strong, to snake L-amino acid oxidase.
                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=BALB/c, and CBA/J;
MEDLINE=97225983; PubMed=9122225; DOI=10.1073/pnas.94.6.2507;
                                                                                                                                                                                                                                                                                                                                                                                     representational difference analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Immunol. 35:487-502(1998).
                                                                                                                                                                                                                                                                                               SEQUENCE OF 122-289 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 217-630 FROM N.A.
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EMBL; U70430; AABS1354.1; -.
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                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                     Paul W.E.;
                                                                                                         NCBI_TaxID=10090;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 FNKHTLLEYLLEEGNLSRPAVQLLGDVMSEBGFFYLSPAEALRAHACLSDRLRYSRIVGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 SDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSYQTGNESSLMDLSADIVLVTTTAKA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 WDLLPRALLSSLSGALLINAPVVSITQGRNDVRVHIATSLHSE-KTLTADVVLLTASGPA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 ALFIDEDPELSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIRGGKSITDGPSRYIYYP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 LQRITFSPPLTRKRQEALRALHYVAASKVFLSFRRPFWHEEHIEGGHSNTDRPSRLIFYP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIHGE---QVWDKCTGV 442
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                                                                                                                                                                                                                                                                                                                                                           R -> Q (in Ref. 3).
PSEHVQVHGEVIPEWHGHGGSGTPQWHRVGDHS -> LRSM
YRCMGKSSLSGMVMGDLAPRKCTEWGTTPNRKEEVSTQLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 AASSLNPIEKCMEDHDYEQLLKVVTLGLNRTSKPQKVVVVGAGVAGLVAAKMLSDAGHKV
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FAD (ADP part) (Potential).
N-linked (GICNAC. .) (Potential).
N-linked (GICNAC. .) (Potential).
N-linked (GICNAC. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.3%; Score 1034; DB 1; Length 63
Best Local Similarity 43.5%; Pred. No. 1.7e-55;
Matches 212; Conservative 100; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                630 AA; 70190 MW; A674C5D60D89A071 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Interleukin-four induced gene-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           OPSSGOTDHLH (in Ref.
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HSSP; P81382; 1F8R.
MGD; MGI:109552; I14i1.
InterPro; IPR000159; Amineoxid fl.
InterPro; IPR001613; Amineoxid fl.
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR0020937; Amino_oxidase.
Ffam; PF01593; Amino_oxidase; I.
PRINTS; PR00419; ADXROTASE.
PRINTS; PR00757; AMINEOXDASEF.
                                                                                                                                                                                                                            Potentia
                                                                                                                                                                                                 FAD; Flavoprotein; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                NCBI_TaxID=10090;
                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 AQGEGS-----LILLASYTWSDAAAPFAGLSTDQTLRLVLQDVAALHGPVVFRLWDG-RGV
                                                                                                                                                                                                                                                                                                                                      26 ALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTV
                                                                                                                                                                                                                                                                                                                                                                                          86 TILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSHRIVQWFVKKLGVEMNEFVMTDDNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 YDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSYQTGNESSLMDLSADIVLVTTTAKA
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                                                                                                                                                                                                                                                                                                              12; Gaps
           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=114i1;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                 Query Match
38.3%; Score 1034; DB 2; Length 630;
Best Local Similarity 43.5%; Pred. No. 1.7e-55;
Matches 212; Conservative 100; Mismatches 163; Indels 1
                                                                                     Chu C.C., Kim J.A., Hsueh K.;

Lu Chu C.C., Kim J.A., Hsueh K.;

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; AYIGI348; AA023118.1;

GO; GO:0006118; P:alectron transport; IEA.

R InterPro; IPR000759; Adrndx reductase.

R InterPro; IPR000537; Amino oxidase.

R InterPro; IPR002037; Amino oxidase.

R InterPro; IPR002037; Amino oxidase.

R PRINTS; PR00419; ANXEDTASE.

R PRINTS; PR00757; AMINEOXDASEF.

SEQUENCE 630 AA; 70162 MW; 667515D60D893955 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequ
05-JUL-2004 (TrEMBLrel. 27, Last anno
Interleukin-4 induced gene-1 protein.
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                                                                 FROM N.A.
                                       NCBI_TaxID=10090;
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                                                                           STRAIN=MRL;
                                                                 SEQUENCE
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06YDI8

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AC 06YDI

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               STRAIN=NZW;
A Chu C.C., Kim J.A., Hsueh K.;
Chu C.C., Kim J.A., Hsueh K.;
Chu C.C., Kim J.A., Hsueh K.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX157538; AA017039.1; -.
EMBL; AX157537; AA017039.1; -.
EMBL; AX157537; AA017039.1; -.
EMBL; AX157537; AA017039.1; -.
EMBL; AX157537; AA017039.1; -.
EMBL; AX157537; AA017038.1; -.
EMBL; AX1575393; AMINEOXID fl.
EINTETPO; IPR001293; AMINEOXID fl.
EINTETPO; IPR002937; AMINEOXID SE.
EPRNINS; PR00419; ADXEDTASE.
EMBLYES; PR00457; AMINEOXDASEF.
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
38.3%; Score 1034; DB 2; Length 6
Best Local Similarity 43.5%; Pred. No. 1.7e-55;
Matches 212; Conservative 100; Mismatches 163; Indels
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ne : 193 secs
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FROM N.A.
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Sequence 2456, Ap Sequence 1224, Ap Sequence 1324, Ap Sequence 17742, A Sequence 4659, Ap Sequence 4659, Ap Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

Sequence 42648, A Sequence 3712, Ap Sequence 7202, Ap Sequence 2, Appli Sequence 122, Appli Sequence 122, Appli Sequence 11910, A Sequence 11910, A Sequence 7130, Ap Sequence 7130, Ap Sequence 7130, Ap Sequence 7130, Ap Sequence 199, Appli

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APPLICANT: HILARY CLARK
APPLICANT: BRISDELL HUNTE
APPLICANT: JANGER K. JACKMAN
APPLICANT: JANGER K. JACKMAN
APPLICANT: JILL SCHORNFELD
APPLICANT: JILL SCHORNFELD
APPLICANT: JILL SCHORNFELD
APPLICANT: WILLIAM I. WOOD
APPLICANT: THOMAS D. WU
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
TITLE OF INVENTION: RELATED DISEASES
FILE REFERENCE: P1975R1-PCT
CURRENT APPLICATION NUMBER: PCT/US03/28361
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-09-11
SENIOR FILING DATE: 2002-09-11
SENIOR: CCT
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PCT-US03-10870-2456
US-10-218-141-1224
US-10-218-141-1324
US-11-097-143-13742
PCT-IB03-06509-4659
US-10-934-893-4659
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US-11-097-143-17202
US-11-097-143-17202
US-10-914-020-7202
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US-10-162-381B-127
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Best Local Similarity 41.8*
Matches 217; Conservative
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APPLICANT: SARAH C. BODARY
APPLICANT: HILARY CLARK
       ; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-28361-44
       PCT-US03-28361-44
       임
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and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US1_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US1_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US1_NEW_COMB.pep:*
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-156-607-84
US-10-166-087B-48
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PCT-USO5-09248-13
PCT-USO3-10870-447
US-10-990-328A-828
US-10-990-328A-828
US-10-990-328A-829
US-10-990-328A-829
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US-11-051-454-250
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Minimum DB Maximum DB

Database

Title: Perfect score:

Run on:

Sequence:

Scoring table:

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Result 8

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APPLICANT:
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ORGANISM:
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APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: DOLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REPRENCE: CLOOL495
CURRENT APPLICATION NUMBER: US/10/990,328A
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1137
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                                                                                             KFWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
                                                                                                                                                   ELALRDLAKIHG----EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
                                                                                                                                                                             -----ALWQTEK 466
                                          QTGNES-SLMDLSADIVLVTTTAKAALFIDFDPLSISKMEALRSVHYDSSTKILLTFRD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
ALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSY
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Best Local Similarity
Matches 217; Conserv
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US-10-990-328A-11737
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SERETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILE REFERENCE: 39870-3330R1C409
CURRENT PELLING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/028,072
PRIOR APPLICATION NUMBER: PET/US00/32678
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR PELLING DATE: 2000-12-01
PRIOR SPELICATION NUMBER: US 60/187,202
NUMBER OF SEQ ID NOS: 550
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--ALWQTEK
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37.0%; Score 999; DB 6; Length 56
Best Local Similarity 41.8%; Pred. No. 1.4e-65;
Matches 217; Conservative 99; Mismatches 171; Indels
  417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQGGFVVQPP-
                                                -----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508
                                                                             DDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN
                                                                                                                                                                                                          Sequence 476, Application US/10152381B
GENERAL INFORMATION:
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Watanabe, Colin K.
Wood, William I.
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Tumas, Daniel
                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Smith, Victoria
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Filvaroff, Ellen
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
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US-10-152-381B-476
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Pred. No. 1.4e-65;

41.8%;

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Best Local Similarity
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                                     362 PFWREEHIEGGKSNTDRPSRMIFYP-----PPREGALLLASYTWSDAAAAFAGLSREEAL 416
                                                                                                                   ----ALWQTEK 466
               KEWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
                                                                                 ELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 84
LENGTH: 567
                                                                                                            417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQGGFVVQPP-
                                                                                                                                                 -----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508
                                                                                                                                                                     PRIOR APPLICATION UNMER: 60/09946,374
PRIOR PILLING DATE: 2001-09-04
PRIOR PLING DATE: 2001-09-04
PRIOR PLING DATE: 1998-09-01
PRIOR PLING DATE: 1998-09-01
PRIOR PLING DATE: 1998-09-01
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PRIOR PLING DATE: 1998-09-02
PRIOR PLING DATE: 1998-09-03
PRIOR PLING DATE: 1998-09-03
PRIOR PLING DATE: 1998-09-09
PRIOR PLING DATE: 1998-09-09
PRIOR PLING DATE: 1998-09-09
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Grimaldi, Christopher
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Fong, Sherman
Gao, Wei-Qiang
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Paoni, Nicholas F.
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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37.0%; Score 999; DB 7; Length 567;

Query Match

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FRAGMENT ENCODING AN NRPS FOR THE BIOSYNTHESIS OF
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                                                                                                                                                     62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH
                                                                                                                                                                                                                                                        122 RIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD
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                                                  3 LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH
                                                                             Gaps
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29.2%; Pred. No. 7.5e-22;
tive 83; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces refuineus subspecies thermotolerans
  Indels
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  Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ecopia Biosciences Inc.
APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: NUCLEIC ACID FRAGMENT ENCY
TITLE OF INVENTION: NUCLEIC ACID FRAGMENT ENCY
TITLE REFERENCE: 3014-2US
CURRENT APPLICATION NUMBER: US/10/166,0878
CURRENT FILING DATE: 2002-06-11
NUMBER: OF SEQ ID NOS: 57
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-166-087B-48; Sequence 48, Application US/10166087B; GENERAL INFORMATION:
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Matches 144; Conservative
217; Conservative
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us-10-645-094-1.rapn

OY 264	Db 383 EBRIKKLCELYAKVLGSLEALBEVHYEEKNWCEEQYSGCYTTYFPGIL 432 QY 467 -EYAQELFSSEGRVHFAGEHTAFPHAWIETSMKSAIRAATNINKVANEE 514 : :		Query Match Best Local Similarity 25.0%; Pred. No. 5.4e-13; Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27; Qy 62 VVIVGAGMAGLTAAKLLODAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRI-PSS 120 T VVVVGGISGMAAAKLLHDSGLNVVVLEARDRVGGRTYTLRNQKVK-YVDLGGSYVGPTQ 65	Qy 121 HRIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVERTYVVQENPDVLKYNVS 171		264GGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSYQTGNESSLMDL	Db 256 EAKYVISAIPPTLGMKIHFNPPLPMMRNQMITRVPLGSVIKCIVYYKEFFWRKKDY-CGT 314 Qy 373 SITDGPSRYIXYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEELKEL 422
166 131 217 186 267 242 327	Db 300 RRVNLSWARLSAAKHAAIRRLRYASTVRVFLQMRRKFWPERRLMLSTDTAVRTVRDATPH 359 Qy 376 -DGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELARDLAKIHG 432	RESULT 6 US-10-940-774A-11442 i Sequence 11442, Application US/10940774A i GENERAL INFORMATION: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF i FILE REFERENCE: CL001307 CURRENT APPLICATION NUMBER: US/10/940,774A i PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 i PRIOR FILING DATE: 2000-10-20 i PRIOR FILING DATE: 2000-10-20 i PRIOR FILING DATE: 2000-10-20 i PRIOR FILING DATE: 2000-10-20	-	US-10-940-774A-11442 Query Match Best Local Similarity 24.9%; Pred. No. 2.1e-13; Matches 133; Conservative 86; Mismatches 176; Indels 140; Gaps 27;	TAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYA 1	FPPV 1 SVKE 2 ::	QY 214 YLKEEGGLSPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVT 263

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477 GRVHFAGEHTAFPH--AWIETSMKSAIRAATNI----NKVANEE
                                                                                                                                                                                                                             Sequence 448, Application PC/TUS0310870 GENERAL INFORMATION:
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25.0%;
                                                                                                                                                                                                                                                                                                                      Buck Institute
Ghosh, Soumitra S.
Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 131; Conservative
                                                                                                                                                                                                                                                                                               APPLICANT: Mitokor, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                             369 AKVLGSLEALEPUHYEE------KNWCEEQYSGGCYTTYFPPGILTQYGRVLRQPV 418
MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL----TKEERLKKLCELY 368
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Chang, Bind,
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERRORE: 660088.465PC
CURRENT APPLICATION NUMBER: PCT/US03/10870
CURRENT PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3025
SOOFWARE: FRRESEQ FOR WINGOWE Version 4.0
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                                                                                                                                                                                     GRVHFAGEHTAFPH--AWIETSMKSAIRAATNI----NKVANEE 514
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 447, Application PC/TUS0310870 GENERAL INFORMATION:
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LENGTH: 520
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62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRI-PSS 120
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NRILR-LAKELGLETYKVNEVER-----LIHHVKGKSYPFRGPFPDVWNP--ITY---
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APPLICANT: Ziang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gibson, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DEBTILED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465PC
CURRENT PAPLICATION NUMBER: PCT/US03/10870
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 520
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                       Sest Local Similarity
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                                       ; ORGANISM: Homo E
US-10-990-328A-8288
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                                                              TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO1495
CURRENT APPLICATION NUMBER: US/10/990,328A
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FASLSEQ for Windows Version 4.0
LENGTH: 520
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REPERBNCE: CL001495
CURRENT APPLICATION NUMBER: US/10/990,328A
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8288
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-10-990-328A-8287
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US-10-990-328A-8288
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF PROSITION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSITION ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSITION ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/11/051,454
CURRENT APPLICATION NUMBER: US/10/205,823
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-07-35
PRIOR FILING DATE: 2001-07-35
PRIOR FILING DATE: 2001-07-35
PRIOR FILING DATE: 2001-07-25
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                                                                     Gaps
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                                                                 Indels 140;
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10.7%; Score 288; DB 6; Lv 25.0%; Pred. No. 5.4e-13; tive 84; Mismatches 169;
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Gorbatcheva, Bella
Hoersch, Sebastian
Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
Zhao, Xumei
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APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O
                                                                 Matches 131; Conservative
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62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH 121
                                                                                                                                                                                                                                                                                                    RIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQE-----NP-DVLKYNVSESE 174
                                                                                                                                                                                                                                                                                                                                 175 KGISADDLLDRALQKVKEEVEANGCKAA--LEKYDRYSVKEYLKEEGGLSPGAVRMIGDL 232
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                                                                                                                                                                                                                                 Gaps
                                                                                                         10.5%; Score 283; DB 1; Length 527; 23.4%; Pred. No. 1.3e-12; Live 91; Mismatches 197; Indels 108;
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APPLICANT: Zhang, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glann, Gary M.
APPLICANT: Glann, Gary M.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088465FC
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: PASESEQ FOR Windows Version 4.0
SEQ ID NO 549
LENGTH: 527
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APPLICANT: Buck Institute
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
                                                                                                       Query Match
Best Local Similarity 23.44
Matches 121; Conservative
                                       Homo sapiens
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PCT-US03-10870-549
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Best Local Similarity
                                       ; ORGANISM: Homor
PCT-US05-09248-11
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APPLICANT: Xu, Jianchao
APPLICANT: Desir, Gary
TITLE OF INVENTION: DETECTION, ISOLATION AND USES OF RENALASE (MONOAMINE OXIDASE OF
TILE OF ILLING DATE: 2005-03-28
CURRENT APPLICATION NUMBER: US 60/554,552
PRIOR APPLICATION NUMBER: US 60/554,552
PRIOR APPLICATION NUMBER: US 60/615,452
PRIOR PILING DATE: 2004-03-19
PRIOR FILING DATE: 2004-03-19
PRIOR PILING DATE: 2004-10-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
LENGTH: 527
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PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR PILING DATE: 2001-12-12
PRIOR PLING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SEQ ID NO 252
LENGTH: 520
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PCT-USOS-09248-11
Sequence 11, Application PC/TUSOS09248
GENERAL INFORMATION:
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US-11-051-454-252
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Best Local Similarity
Matches 131; Conserv
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GENERAL INPORMATION:
GENERAL INFORMATION:
FOLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001495
                                                                                                                                                                                                                                                                                                                                                                                                                                             432
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 18
                                                                                                                                                                                                                                                           175 KGISADDLLDRALQKVKEEVEANGCKAA--LEKYDRYSVKEYLKEEGGLSPGAVRMIGDL 232
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                                                                                                                                                                                                                                                                                                                           220 VGGSGQVSERIMDLLGDQVKLNHPVTHVDQSSDNIIIE-TLNHEHYECKYVINAIPPTLT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQVWDKCTGVIVKKWSADPYSLGAF-ALFTPYQHLEYAQELFSSEGRVHFAGEHTA---- 487
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                                 62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH 121
                                                                                                   122 RIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQE-----NP-DVLKYNVSESE 174
                                                                                                                                                                                                                                      AKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIRGGKSITDGPSRYI 382
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                                                   16 VVVIGGGISGLSAAKLLTEYGVSVLVLEARDRVGGRTYTIRNEHVDYVDVGGAYVGPTQN
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91; Mismatches 197; Indels 108;
                                                                                                                                                                                                    ----NLWRTIDNMGKEIPTDAPWEAQHADKWDKMTMKE---
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121; Conservative
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US-10-990-328A-8290
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US-10-990-328A-8290
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                                                                                                                                                                                                      220 VGGSGQVSERIMDLLGDQVKLNHPVTHVDQSSDNIIIE-TLNHEHYECKYVINAIPPTLT
                                    161 IDKICWTKTA-RRFAYLFVNINVTSEPHEVSALWFLWYVKQCGGTTRIFSVTNGGQERKF
                                                                                  -GGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSYQTGNESSLMDLSADIVLVTTT
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LNEQSLMYTALSEMIYDQADVNDSVTYHEVT
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Job time : 81 secs
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Ada 45995 Ada 16426 Ada 1699 Adb 1948 4 Adb 2025 Ada 6025 Ada 4768 Ada 4768 Ada 3764

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1 MNLHVVKWKLSVVSVLITLYYSHTVALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell death; apoptosis; inhibition; proliferation; cancer cell; apoptosis inducing protein; AIP; chub mackerel; anticancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis inducing protein from mackerel and
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ADB28025
ADB166504
ADB166504
ADB47854
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1 MNLHVVKWKLSVVSVLITLY......TNINKVANEESTIEHTKDEL 524
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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                                                                                                                                                     TALSEMIYDQADVNDSVTYHEVTGGSDLLPEAPLSVLDVPILLNSKVKHIRQSDKGVIVS
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                                         HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGMYAEMGAMRIPSS
                                                                 HRIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISAD
                                                                              HIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISAD
                                                                                                      DLLDRALOKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMY
                                                                                                                        DLIDRALQKVKEEVBANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLINEQSLMY
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N-PSDB; ADO60381.
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amino acid oxidase having a fully defined amino acid sequence of 523 amino acids as given in the specification and L-amino acid oxidase activity. The invention may be useful for the production of compounds with an antibacterial activity. The invention is useful in preparing an antibacterial sterilisation composition as a hydrogen peroxide supply component. The invention is useful for preventing, treating bacterial infections such as sexually transmitted disease in the breast of livestock, for example mastitis, and provides an antimicrobial effect. The present sequence is that of the mouse L-amino acid oxidase protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVT
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Pred. No. 1.9e-74;
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                                                                                                                                                                                                                                                                                                                      Sequence 523 AA;
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note= "a mitochondrial localisation motif is near Gln22"
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384 ARGEGS----LLLASYTWSDAAAPFAGLSTDQTLRLVLQDVAALHGPVVFRLWDG-RGV
                                                            IVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE-GRVHFAGEHTAFPHAWIETSMKSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated genes from human dendritic cells - which encode products having disintegrin-metallo-proteinase mono:amine oxidase or GTPase
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Disintegrin metalloproteinase; proteinase; BS10.55; human.
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358. .390
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52. .78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide, which encodes a human immediate early interleukin-four (IL-4) induced protein. The activity of the polynucleotide of the invention may be described as cytostatic, antifungal, antibacterial, immunomodulator, antiinflammatory, dermatological and immunosuppressive. The polynucleotide or antisense of Algonucleotide is useful for the manufacture of a medicament for preventing, treating or ameliorating a medical condition, particularly immune related disease, tumour, fungal infection or bacterial infection. The immediate early IL-4 induced protein is useful for the manufacture of a medicament for killing unwanted cells in a mammal. The antagonist is a useful for the manufacture of a medicament for killing unwanted cells in a mammal. The antagonist is cuseful for the manufacture of a set in decreasing cell condition, particularly an immune related disease. These diseases may condition, particularly an immune related disease. These diseases may condition battenic lupus erythematosus, inflammatory bowel disease, condition. Battenic lupus erythematosus, inflammatory bowel disease, dullain-Batter syndrome, Whipple's disease, atopic dermatitis, food hypersensitivity, rheumatoid arthritis, osteoarthritis, diabetes mellitus and psoriasis. The polynucleotide of the invention may be used in gene therapy. The current sequence represents the mouse immediate early
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 ALFIDFDPPLSISKMBALRSVHYDSSTKILLTFRDKFWBDDGIRGGKSITDGPSRYIYYP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIHGE---QVWDKCTGV 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 AASSLNPIEKCMEDHDYEQLLKVVTLGLNRTSKPQKVVVVGAGVAGLVAAKMLSDAGHKV 84
                                                                                                                                                                                                                                                                                              New human immediate early interleukin-four (IL-4) induced protein and polynucleotides, useful for preventing or treating immune related disease, tumor, fungal or bacterial infection, e.g. lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYLVNGVRERTYVVQENPDVLKYNVSESEKGISADDLLDRALQKVKEEVEANGCKAALEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 LQRITFSPPLTRKRQEALRALHYVAASKVFLSFRRPFWHEEHIEGGHSNTDRPSRLIFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 ALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.3%; Score 1034; DB 5; Length 6. Best Local Similarity 43.5%; Pred. No. 3.4e-73; Matches 212; Conservative 100; Mismatches 163; Indels
                                                                                                                                                                         (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7(vii); Page 4; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-four induced protein
                                                                                                                                                                                                                     Мавоп ЈМ;
                                                                                                                                 25-AUG-2000; 2000US-0227818P.
                                                                                            24-AUG-2001; 2001WO-US026462
                                                                                                                                                                                                                                                                                                                                                             or Whipple's disease
                                                                                                                                                                                                                   Chavan SS,
                                                                                                                                                                                                                                                         WPI; 2002-329772/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 630 AA;
                WO200218574-A2
                                                      07-MAR-2002
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 translation product does not have the key residues which covalently bind the PAD cofactor. and so may not exhibit monoamine oxidase activity. The cellular types which express messages encoding YFF03 suggest that signals important in cell differentiation and development are mediated by them. The invention provides a process for recombinant production of YFF03, host cells, expression vectors and specific antibodies. The products can be used for detection, diagnosis, development of therapeutic methods and
                                                                                                                                                                                                                                                                                                           241
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                                                                                                                                                         LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH 61
                                                                                                                                                                                                                                                                                               182 IYQMALNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFYL
                                                                                                                                                                                                             ETSPPARNLKVLKADVVLLTASGPAVKRITFSPPLPRHMOEALRRLHYVPATKVFLSFRR
                                                                                                                                                                                                                                                                                                                                                                                                                           362 PFWREEHIEGGHSNTDRPSRMIFYP-----PPREGALLLASYTWSDAAAAFAGLSREEAL
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-----ALWOTEK
                                                                                                                                                                        VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH
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                                                                                                                                                                                                                                                                                                                            242 ALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSY
                                                                                                                                                                                                                                                                                                                                                                                                             KFWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE-
                                                                                                                                       Gaps
                                                                                                                                       32;
                                                                                                                 Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO1265; UNQ636; cancer; tumour; diagnosis; therapy; human.
                                                                                                               37.0%; Score 999; DB 2; Length 56
41.8%; Pred. No. 1.8e-70;
ive 99; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 RLALDDVAALHGPVVROLWDG-TGV-VKRWAEDOHSOGGFVVOPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505
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/note= "signal peptide"
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                                                                                                                          Local Similarity 41.8 les 217; Conservative
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/note=
                                                                                             Sequence 567 AA;
                                                                        drug screening
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against proteins expressed in neoplastic cells, useful for tumor
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Amplification of DNA60764 occurs in various lung and colon tumours and cell lines, suggesting a significant role in tumour formation and growth Antagonists (e.g. antibodies) directed to PRO1265 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAV06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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LHL----LVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roy
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    /note= "homology to D-amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.0%; Score 999; DB 2; L. Llarity 41.8%; Pred. No. 1.8e-70; Conservative 99; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillan KJ,
                                                                                 220...223
/note= "Asn is N-glycosylated"
559...56
/note= "Asn is N-glycosylated"
                                                            /note= "Asn is N-glycosylated"
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98US-0083500P.
98US-0086414P.
98US-008742P.
98US-0107783P.
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es 217; Conserv
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                                     Modified-site
                                                                                 Modified-site
                                                                                                                             Modified-site
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22-MAY-1998;
10-JUN-1998;
10-NOV-1998;
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Wood WI;
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   362 PFWREBHIEGGHSNIDRPSRMIFYP-----PPREGALLLASYTWSDAAAAFAGLSREEAL 416
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                                                                                               KFWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
242 SFAEALRAHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI 301
                                QTGNES-SIMDLSADIVLVTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO1265 (UNQ636) amino acid sequence SEQ ID NO:84.
                                                                                                                                                                                                                            -----GRVHPAGEHTAFPHAWIETSWKSAIRAATNIN 508
                                                                                                                                                                                                                                                                                                                                               AAY99364 standard; protein; 567 AA
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421 ELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                              "Tyrosine kinase phosphorylation site"
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161. .169
/note= "Tyrosine kinase phosphorylation site"
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                                -----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508
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/note= "D-amino oxidases proteins
                                                                                         DDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN
                                                                                                                                                                                                                                                         Amino acid sequence of novel polypeptide PRO1265.
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/note= "N-glycosylation site"
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e= "transmembrane domain"
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                                                                                                                                                                         AAY93687 standard; protein; 567
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/note= "N
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Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
                                                                                                                                                                                                                                                                                                                                             small
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                                                                                                                                                                                                                                                                                                                                         New mammalian DNA sequences encoding transmembrane, receptor or s
PRO polypeptides, useful for screening of potential peptide or sn
molecule inhibitors of the relevant receptor/ligand interactions
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41.8%; Pred. No. 1.8e-70;
ive 99; Mismatches 171; Indels
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                                                                                                                                                                                                                                                                       Smith V,
                                                                                                                                                                                                                                                                          Gurney AL,
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98US-0108779P.
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Matches 217; Conservative
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                             specification describes novel polypeptides designated PRO201, PRO292, PRO312, PRO1015, PRO1017, PRO313, PRO1017, PRO1017, PRO1017, PRO1012, PRO1017, PRO5101, PRO509, PRO503 and PRO502. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognesis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in
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                                                                                                                                                                                                                                                                                            LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH
                                                                                                                                                                                                                                       VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH
                                                                                                                                                                                                                                                          VIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSH
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                                                                                                                                                                            32;
                    present sequence represents a novel human polypeptide.
                                                                                                                                                                          99; Mismatches 171; Indels
                                                                                                                                                        Length
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                                                                                                                                                       37.0%; Score 999; DB 3; 41.8%; Pred. No. 1.8e-70;
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Claim 61; Fig 8; 220pp; English
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                                                                                                                                                    Query Match
Best Local Similarity 41.8
Matches 217; Conservative
                                                                                                                                    Sequence 567 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 ALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                     Fong S;
Hillan KJ;
Watanabe C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense KNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nuclacids may also be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFAEALRAHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 RIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to secreted and transmembrane proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful as hybridization probes, in chromosome and gene mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane proteins and nucleic acids designated
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Gurney AL, 1
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                                                                                                                                                                                                                                                                                                                                                     noyers L, Eaton DL, F
I PJ, Grimaldi CJ, Gu
Smith V, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                   er KP, Botstein D, Desnoyers
W, Goddard A, Godowski PJ,
J, Paoni NF, Roy MA, Smith
liams PM, Wood Wi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 50; 787pp; English.
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                                                                                                                                                             99WO-USO28313.
99WO-USO28551.
99WO-USO30095.
2000WO-US000219.
                                                               99US-0144758P.
99US-0145698P.
99WO-US020111.
2000WO-US004342
                                            99US-0141037P
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Similarity 41.8%;
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                                                                                                                                                                       Human; PRO1265; antiinflammatory; dermatological; immunosuppressive; antirheumatic; antiarchritic; osteopathic; antianaemic; haemostatic; antithyorid; antidiabetic; antiviral; antipsoriatic; antiallergic; antiatergic; antiatergic; antiatergic; antiatergic; antiatergic; antiatergic; antiatergic; antiatergic; spondyloarthropathy; systemic sclerosis; systemic vasculitis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; autoimmune thrombocytopenia; immune-mediated renal disease; hepatitis; demyelinating polyneuropathy; Guillian-Barre syndrome; Whipple's disease; hepatobiliary disease; primary biliary cirrhosis; sclerosing cholangitis; inflammatory bowel disease; gluten-sensitive enteropathy; skin disease; allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria; eosinophilic pneumonia; hypersensitivty pneumonitis; graft rejection; idiopathic pulmonary fibrosis; graft-versus-host-disease.
RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQGGFVVQPP-----ALWQTEK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Asn is N-glycosylated"
61. 169
'label= Tyrosine_kinase_phosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                                                       label= Tyrosine_kinase_phosphorylation_site
                                                                                                                                                      Human PRO1265 protein encoded by DNA60764-1533 cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                         22. .567
/label= Mature_human_PRO1265_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ii. 81
/label= D-amino_acid_oxidase_protein
                   -----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508
                               DDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505
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re= "Asn is N-glycosylated"
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130. .136
/note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                      .. .21
'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                         AAY72874 standard; protein; 567
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/note= "N
'59
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/note= "N-
                                                                                                                                  (first entry)
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                   477
                                        467
                                                                                                                                                                                                                                                                                                                                                                         Protein
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une present sequence is rectain encoura by whose particles of the antibody which are capable of enhancing or inhibiting the proliferation of T-lymphocytes or of increasing the infiltration of inflammatory cells into a tissue are useful in the diagnosis and treatment of immune-related diseases in mammals. The PRO protein is useful for treating systemic lupus exthritis, spondyloarthropathy, systemic solerosis, idiopathic arthritis, structure, spondyloarthropathy, systemic solerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, arthritis, autoimmune harmonlytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating disease of the central or peripheral nervous system, chippathic demyelinating polymeuropathy, hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, seleosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Mhipple's disease, autoimmune-mediated skin disease, skin disease, autoimmune-mediated skin diseases and sensitive enteropathy sould a bullous skin disease, autoimmune-mediated skin disease, skin disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erythema multiforme and contact dermatitis, psoriasis, allergic diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides for treating immune related and inflammatory diseases such as rheumatoid arthritis, systemic vasculitis, asthma, autoimmune hemolytic anemia, and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is PRO1265 protein encoded by DNA60764-1533
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                                                                                                                                                                                                                                                                                                               Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       graft rejection or graft-versus-host-disease
                                                                                                                                                                                                                                                                                                               Gurney AL,
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2000WO-US004342.
2000WO-US005601.
                                                                                          2000WO-US013705.
2000WO-US014042.
                                                                                                                                                    2000WO-US014941.
                                                                2000WO-US008439.
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                                                                                                                                                                                                                                                                                                            Godowski PJ
, Wood WI;
                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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CK,
18-FEB-2000;
01-MAR-2000;
30-MAR-2000;
                                                                                                                                                                                           05-JUN-2000;
                                                                                          17-MAY-2000;
                                                                                                                              22-MAY-2000;
                                                                                                                                                              30-MAY-2000;
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Matches 217; Conservative
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antiinflammatory; antianglogenic; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunological disorder.
                      OTGNES-SLMDLSADIVLVTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD
                               ELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE-
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Wood WI;
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Watanabe CK,
                                                                                                                                                              AAB50962 standard; protein; 567
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99US-0141037P.
99US-0144758P.
99WO-US020111.
99WO-US02654.
99WO-US02813.
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99US-0170262P.
99WO-US030095.
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02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000US-0187202P.
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                                                                                                                                                                                                         Human PRO1265 protein.
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N-PSDB; AAC91564.
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09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
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01-DEC-1999;
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23-JUN-1999
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Twenty eight nucleic acids encoding PRO!polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders.
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                                                                                                                                                                                                        The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, contral nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD
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LHL----LVLVPILLLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH
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                                                                                                                                               24; 188pp; English
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Gaps

61 63 181

181 241

121

241

301

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polypeptide expression in a cell sample to that in a control sample. Some
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| ::| | ||:||:||:|| ETSPPARNLKYLKADVVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRR 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 ELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
             of the 275 sequences are also useful to stimulate the release of tumour differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of Thymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCS), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor vIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polypucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                     62 VIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSH
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                                                                                                                                                                                                                                                                       Length 567;
                                                                                                                                                                                                                                                                     37.0%; Score 999; DB 4; Length 56
41.8%; Pred. No. 1.8e-70;
ive 99; Mismatches 171; Indels
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                                                                                                                                                                                                                                                                                       Similarity
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ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU12172-AAU1246 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Tumas D,
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2000WO-US005841.
2000US-0187202P.
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2000WO-US013705.
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2000US-0209832P.
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99US-0170262P
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99WO-US030911
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2000WO-US000277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides, and detect tl
breast, prostate, cervical
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ME, Goddard
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Stewart TA,
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                                                                             WO200140466-A2
                                              Homo sapiens
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02-DEC-1999;
09-DEC-1999;
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Gaps

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ALSEMIYDQADVNDSVTYHEVTGGSDLLPEÅFLSVLDVPILLNSKVKHIRQSDKGVIVSY 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                    3 LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH
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                                                                                                                                                                    37.0%; Score 999; DB 5; Length 567; 41.8%; Pred. No. 1.8e-70; ative 99; Mismatches 171; Indels
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                           Local Similarity
hes 217; Conserv
                                                                                                                           Sequence 567 AA;
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Matches
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rheumatoid arthritis; myocardial infarction; thrombophlebitis;
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
wound healing; chromosome mapping; gene mapping.
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,, Hillan KJ, Marsters SA, Pan J,
:K, Williams PM, Wood WI, Ye W;
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28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
14-MAR-2001; 2001US-008082706.
12-MAR-2001; 2001US-00808689.
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2000WO-US023328.
2000US-0230978P.
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2000WO-US032678.
2000US-00747259.
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05-APR-2001; 2001US-0082836.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
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2000US-0242922P.
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24-OCT-2000;
08-NOV-2000;
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24-AUG-2000;
07-SEP-2000;
18-SEP-2000;
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24-AUG-2000;
07-SEP-2000;
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                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynuclectide, which encodes a chuman immediate early interleukin-four (IL-4) induced protein. The activity of the polynuclectide of the invention may be described as, cytostatic, antifungal, antibacterial, immunomodulator, antiinflammatory, communosuppressive. The polynuclectide or antisense oligonuclectide is useful for the manufacture of a medicament for immuno ralated disease, tumour, fungal infection or bacterial infection. The immediate early IL-4 induced protein is useful for the manufacture of a medicament for killing unwanted cells in amammal. The antagonist is useful for the manufacture of a medicament for wasted in a medicament for whilm unwanted cells in a mammal. The antagonist is useful for the polynuclectide is also useful for diagnosing a pathological condition, particularly an immune related disease. These diseases may condition, particularly an immune related disease. These diseases may condition, particularly an immune related disease. These diseases may condition, particularly an immune related disease. The polynuclectide is also useful for the manufacture of a medicament to the inventitis, diabetes mallitus condition, particularly rheumatosus, inflammatory bowel disease. The polynuclectide of the invention may be used in gene tharvany the curvent seminar removerents a human immediate early.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 ALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPAEALRAHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy. The current sequence represents a human immediate early interleukin-four induced protein. Note: This sequence should be encoded by the DNA sequence given in the specification as SEQ ID 3 (Human immediate early interleukin-four induced protein genomic DNA from chromosome 19q13.3-19q13.4 - see ABL56822), however, this does not appear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 RIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 VIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRWBSSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                          New human immediate early interleukin-four (IL-4) induced protein and polynucleotides, useful for preventing or treating immune related disease, tumor, fungal or bacterial infection, e.g. lupus erythematosus or Whipple's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 LLDRALQKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 41.8%; Pred. No. 1.88-70;
Matches 217; Conservative 99; Mismatches 171; Indels
                                       (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES
                                                                                                                                                                                                                                                                    Claim 1(a); Page 5; 61pp; English
                                                                                  Mason JM;
25-AUG-2000; 2000US-0227818P.
                                                                                                                         WPI; 2002-329772/36.
                                                                                  Chavan SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to be the case
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Human, angiogenesis, PRO protein, cardiovascularisation; wound; cancer; atherosclerosis, cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic.
421 BLALRDLAKIHG----EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLBYAQELFSSE- 476
                                         .----ALWQTEK 466
                                                                                                                                                                                                                                                                                                                                   Human angiogenesis related protein PRO1265 SEQ ID NO: 176.
                          467 DDWIVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505
                                                                                    -----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN
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                                                                                                                                                                                                                        ABB95510 standard; protein; 567
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2000US-0222695P.
2000US-00643657.
2000WO-US023522.
2000WO-US023328.
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20-JUN-2001; 2001WO-US019692
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2000WO-US034956.
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2001US-00816744.
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2001WO-US017092
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2001US-00854208
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                                                                                                                                                                                                                                                                                                      19-JUL-2002 (first entry)
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FERRARA N.
GERBER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200208284-A2
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14-MAR-2001;
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99WO-US030720
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02-JUN-1999;
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                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFAEALRAHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 PFWREEHIEGGHSNTDRPSRMIFYP----PPREGALLLASYTWSDAAAAFAGLSREEAL 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerber H, Gerritsen ME, Goddard A;
,, Hillan KJ, Marsters SA, Pan J, Paoni NF;
.K, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH
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                                                                                                                                                                                                                                                     One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.0%; Score 999; DB 5; Length 56
41.8%; Pred. No. 1.8e-70;
ive 99; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                          Claim 11; Fig 176; 567pp; English.
                                                                                                                                                                             Gurney AL,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 41.8
Matches 217; Conservative
                     GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
PAN J.
GERRITSEN M E.
                                                                                                STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
WOOD W I.
                                                                                                                                                                   Ferrara N,
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N-PSDB; ABL95648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 567 AA;
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                                                                                                                                                                                           Stephan JF,
                                                                                                                                                                 Baker KP,
Godowski P
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(WOOD/)
                                                              MARS/)
                                                                          (PANJ/)
                                                                                    PAON/)
                                     (GURN/)
                                                  (HILLL/)
                       (2000)
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gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
TNF-alpha release; cell proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted and transmembrane protein; PRO; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                              Novel human secreted and transmembrane protein PRO1265
                           467 DDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505
-----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508
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                                                                                                                                                                                   ABO17853 standard; protein; 567
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98WO-US019093
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98WO-US019177
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98WO-US024855.
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Godowski
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            2000WO-US000376
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Stewart TA,
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                                                                                       10-NOV-2000;
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New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency
Gao W;
                           y AL, Sherwood S;
Wood WI, Zhang Z
Deforge L, Desnoyers L, Filvaroff E,
                               A, Godowski PJ, Gurney
Tumas D, Watanabe CK, W
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Search completed: October 4, 2005, 14:03:38

time : 170 secs

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has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding colypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (1) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a context of the prolypeptide modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF) alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate or inhibit the uptake of glucose or free fatty acid by cells, stimulate or inhibit the presence of tumour in a mammal. The nucleic from peripheral blood monouclear cells, inhibit the binding of A-peptide from peripheral blood monouclear cells, inhibit the binding of A-peptide codid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, chart defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and cransmembrane PRO polypeptide.
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                                                                                    invention describes an isolated nucleic acid (I) comprising, or which
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US-09-812-694B-25
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US-09-352-159-33
US-09-352-159-33
US-09-352-159-6
US-09-352-159-6
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ALIGNMENTS

300 120 180 240 300 KFWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420 9 9 MNLHVVKWKLSVVSVLITLYYSHTVALSLKBHLADCLEDKDYDTLLQTLDNGLPHINTSH HVVIVGAGMAGLTAAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSS 121 HRIVQWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISAD 241 TALSEMIYDQADVNDSVTYHEVTGGSDLLPBAFLSVLDVPILLNSKVKHIRQSDKGVIVS YQTGNESSLMDLSADIVLVTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSS TALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVS 1 MNLHVVKWKLSVVSVLITLYYSHTVALSLKØHLADCLEDKDYDTLLQTLDNGLPHINTSH HRIVQMFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISAD DLLDRALQKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMY FOR INDUCING .; 0 Length 524; Sequence 1, Application US/09230388

Patent No. 6291644

GENERAL INFORMATION:

APPLICANT: Imanoto, Mitsunori; Jung, Sang-Kee

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR

TITLE REFERENCE: 4703/0F214

CURRENT APPLICATION NUMBER: US/09/230,388

CURRENT FILING DATE: 1999-01-22

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 2 tch
al Similarity 100.0%; Score 2704; DB 3;
al Similarity 100.0%; Pred. No. 3.6e-239;
524; Conservative 0; Mismatches 0; SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1 LENGTH: 524 TYPE: PRT ; ORGANISM: Scomber japonicus US-09-230-388-1

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USA
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1 MNLHVVVKWKLSVVSVLITLYYSHTVALSLKEHLADCLEDKDXDTLLQTLDNGLPHINTSH
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                                                                                                                                                                                                                   Sequence 1, Application US/09912176
; Sequence 1, Application US/09912176
; Patent No. 664973
; GENERAL INFORMATION:
; APPLICANT: Iwamoro. Mitsunori; Jung, Sang-Kee
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS
; FILE REFERENCE: 4703/09214
; CURRENT APPLICATION UNMER: US/09/912,176
; CURRENT FILING DATE: 2001-07-24
; PRIOR PILING DATE: 2001/07/24
; PRIOR PILING DATE: 1999-01-22
; PRIOR PILING DATE: 1999-02-22
; NUMBER OF SEO ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 524
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ORGANISM: Scomber japonicus
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US-09-912-176-1
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                                                                                                                                                                                                                                            APPLICANT: Lebecque, Serge J.E.
APPLICANT: Liu, Yong-Jun
APPLICANT: Dowling, Lynette M.
APPLICANT: Dowling, Lynette M.
APPLICANT: Gorman, Daniel M.
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: MAWMALIAN PROTEINASES; OXIDOREDUCTASES;
TITLE OF INVENTION: RELATED REAGENTS
WUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.0%; Score 999; DB 3; Length 567; 41.8%; Pred. No. 9.3e-83;
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Version #1.30
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MEDIUM TYPE: Floppy disk
COMPUTER: ISMP OF COMPACTION
COMPUTER: ISMP COMPACTION
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COMPUTER: ISM PC CASTERNICHON NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
RECISTRATION NUMBER: SF0693
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-652-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DNAX Research Institute
STREET: 901 Callfornia Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                 ; Sequence 4, Application US/08813150; Patent No. 6069229
                                                                                                                                                                                                                             APPLICANT: Mueller, Christopher
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amino acid
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Best Local Similarity 41.8<sup>†</sup>
Matches 217; Conservative
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362 PFWREEHIEGGHSNTDRPSRMIFYP----PPREGALLLASYTWSDAAAAFAGLSREEAL 416
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                                                                                                      62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH
                         LLDRALOKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMYT
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                                                                                 RIVOMPVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins FILE REFERENCE: P2030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1000-01-13
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: 0C/099/15849
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1999-07-15
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EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VOY: 2.0
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Best Local Similarity 41.4%;
Matches 215; Conservative 99
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ORGANISM: Homo sapiens
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                      OTGNES-SLMDLSADIVLVTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360
                                                                             KFWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
                                                                                                                                                            ELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
                                                                                                                                                                                                417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQGGFVVQPP-----ALWQTEK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Muchaeler, Christopher
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Liu, Yong-Jun
APPLICANT: Liu, Yong-Jun
APPLICANT: Huffine, Constance M.
APPLICANT: Huffine, Constance M.
APPLICANT: Huffine, Constance M.
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: MAWMALIAN PROTEINASES; OXIDOREDUCTASES;
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.0%; Score 999; DB 4; Length 567; Best Local Similarity 41.8%; Pred. No. 9.3e-83; Matches 217; Conservative 99; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTING SIZEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,553
FILING DATE: 10-APR-2000
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/813,150
FILING DATE: 07-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLAST INFORMATION:
NAME: CLAST OF UNMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 35,090
REERRENCE/DOCKET UNMBER: SP0693
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                        477 -----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508
                                                                                                                                                                                                                                                            467 DDWTVPYGRIYFAGEHTAYPHGWVBTAVKSALRAAIKIN 505
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STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09546553
Patent No. 6518405
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
TYPE: amino acids
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62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH 121
62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
18.1%; Score 488.5; DB 4;
Best Local Similarity 33.6%; Pred. No. 2.6e-36;
Matches 112; Conservative 69; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 71 Human Secreted Proteins FILE REFERENCE: P2030P1
CURRENT APPLICATION VUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1999-07-14
EARLIER PRILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
SARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                        302 QTGNES-SLMDLSADIVLVTTTAKAALFIDFDP 333
                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (320)
; OTHER INFORMATION: Xaa equals stop translation
US-09-482-273-194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 194, Application US/09482273 Patent No. 6534631
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: SITE
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                  421 BLALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                    362 PFWREEHIEGGHSNTDRPSRMIFYP----PPREGALLLASYTWSDAAAFAGLSREEAL 416
                                                                                                                                                                                                                                                                                                                                                                                             |: :|
----ALWOTEK 466
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                                                                      242 ALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSY 301
                                                                                                                                                      242 SFAEALRAHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI 301
                                                                                                                                                                                                            QTGNES-SLMDLSADIVLVTTTAKAALFIDFDPLSISKMEALRSVHYDSSTKILLTFRD 360
                                                                                                                                                                                                                                     :| : :| || || :| || || 302 ETSPPELPRHWQEALRRLHYVPATKVFLSFRR 361
                                                                                                                                                                                                                                                                                       361 KFWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
                                                  LIDRALQKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMYT 241
          RILHKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGYALRPQEKGHSPED 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATI: Rosen et al.
APPLICATI: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PS030P1
CURRENT PILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: DCT/US99/15849
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
NUMBER OF SEQ. ID NOS: 267
SOFTWARE: PALENTIN VEY: 2.0
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NAME/KEY: SITE
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Best Local Simi:
Matches 112;
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US-09-482-273-267
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LENGTH: 319
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                                                                                                                                                                     242 ALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLLNSKVKHIRQSDKGVIVSY 301
                                                                                                                                                                                                                                                               SFAEALRAXSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                       181
           84
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                                                  RIVOMFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD
                                                                                85 RILHKLCQGLGLNLTKFTQYDKNTWTEVHEXKLRNYVVEKVPEKLGYALRPQEKGHSPED
----VT1LEADNRIGGRIFTYRDQXTGWIGELGAMRMPSSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring
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216 KEEGGLSPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 ---IPSSHRIVQWFVKKLGVEMNEFVMTDDNTFYLVN-----GVRERTYVVQENPDVLK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 YNVSESEKGISADDLLDRALQKV-----KEEVEANGCKA--ALEKYDRYSVKEYLKEE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 G--GLSPG----AVRMIGDLLNEQSLMYTALSEMIYDQADVNDSV--TYHEVTGGSDLLP 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 GPKGEAPKYDFFAIQWMETQNTGTNLFDQAFSESVIDSFDFDNPTKPEWYCIEGGTSLLV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 EAFLSVLDVPILLNSKVKHIR----QSDKGVIVSYQTGNESSLMDLSADIVLVTTTAKAA 326
                                                                                                       276 VLDVPILLNSKVKHIRQSDKGVIVSYQTGNES-SLMDLSADIVLVTTTAKAALFIDF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 VVIVGAGMAGLTAAKLLQD---AGHTVTILBANDRVGGRVET--YRNEKEGWYAEMGAMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                           APPLICANT: Isaac, Barbara G.
APPLICANT: Greenplate, John T.
APPLICANT: Greenplate, John T.
APPLICANT: Burcell, John P.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: INSECTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: PO Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/99/063,733A FILING DATE: 21-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 417; DB 3; L, Pred. No. 2.7e-29; 83; Mismatches 177;
                                                                                                                                                                                                                       , Sequence 46, Application US/09063733A
, Patent No. 6372211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/ACENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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Best Local Similarity
Matches 156; Conserval
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STRANDEDNESS: not
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                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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CITY: Houston
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USA
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                                                                                                                                        122 RIVOWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD 181
                                                            182 LLDRALQKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMYT 241
                                                                                                                                                                                                 242 ALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equals any of the naturally occurring L-amino acids
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INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (192)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-482-273-265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 TYVVQENPDVLKYNVSESEKGISADDLLDRALQKVKEEVEANGCKAALEKYDRYSVKEYL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --VTILEADNRIGGRIFTYRDQXTGWIGELGAMRMPSSH 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Gaps
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                                                                                                                                                                                                                                                                                                    302 OTGNES-SLMDLSADIVLVTTTAKAALFIDFDP 333
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Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
SEARLIER FILING DATE: 1998-07-15
SCFTWARE: PALCATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
SCFTWARE: PALCATION NOWER: 207
SCFTWARE: PALCATION NOWER: 207
SCFTWARE: PALCATION NOWER: 207
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62; Mismatches
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Best Local Similarity 34.7'
Matches 103; Conservative
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NAME/KEY: SITE
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OTHER INFO
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IBM PC compatible
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TELEBRONE: 713-787-1400
TELEBRAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 617 amino acids TYPE: amino acid
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OPERATING SYSTEM:
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TOPOLOGY: linear
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STREET: FC.
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TOPOLOGY:
US-09-063-733A-57
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US-09-063-733A-57
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                                                                                                                                         424 IRTCVYPSYNLDDTGE--AVLLASYTWSQDATR-IGSLVKDAPPQPPKEDELVELILQNL 480
                                                                                                                                                                                                                   481 ARLHABHMTYEKIKEAYTGVYHAYCWANDPNVGGAFALFGPGQFSNLYPYLMRPAAGGKF 540
                                                                    368 LDRMDLRGLNLHP----TQADAIRCLHYDNSTKVALKFSYPWWIKDCGITCGGAASTDLP 423
                                                                                                                    ----SDEELKELALRDL 427
                                                                                                                                                                                      AKIHG-----EQVWDKCTGVI-VKKWSADPYSLGAFALFTPYOHLEYAQELF--SSEGRV 479
L-----FIDFDPPLSISKMEALRSVHYDSSTKILLIFRDKFW-EDDGIR-GGKSITDGP 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 VVIVGAGMAGLTAAKLLOD---AGHTVTILEANDRVGGRVET--YRNEKEGWYAEMGAMR
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Isaac, Barbara G.
APPLICANT: Greenplate, John T.
APPLICANT: Purcell, John P.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: INSECTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.0%; Pred. No. 2.7e-29;
Matches 156; Conservative 83; Mismatches 177; Indels
                                                                                                                      379 SRYIYYPSHSF-HTNETIGVLLASYTWSDESLLFLGA----
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FILING DATE: 21-APR-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                          480 HFAGEHTAFPHAWIETSMKSAIRA 503
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REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                            E: Arnold White & Durkee
PO Box 4433
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/09063733A Patent No. 6372211
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TELEPAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-063-733A-56
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AKIHG-----BQVWDKCTGVI-VKKWSADPYSLGAFALFTPYQHLEYAQELF--SSEGRV 479
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                                             168 YNVSESEKGISADDLLDRALQKV-----KEEVEANGCKA--ALEKYDRYSVKEYLKEE 218
                                                                         271 EAFLSVLDVPILLNSKVKHIR----QSDKGVIVSYQTGNESSLMDLSADIVLVTTTAKAA
                                                                                                                                                                                                                                                                                                          327 L-----FIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFW-EDDGIR-GGKSITDGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/09063733A
Patent No. 637211
GENERAL INFORMATION:
APPLICANT: Great, Barbara G.
APPLICANT: Great, John T.
APPLICANT: Purcell, John P.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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21-APR-1998
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: PO Box 4433
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STRANDEDNESS:
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                                                                                                                                    TOPOLOGY:
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                                                                 62 VVIVGAGMAGLTAAKLLQD---AGHTVTILEANDRVGGRVET--YRNEKEGWYAEMGAMR 116
                                                                                                 VCIVGAGVSGLYIAMILDDLKIPNLTYDIFESSSRTGGRLYTHHFTDAKHDYY-DIGAMR 145
                                                                                                                                                 253 GPKGEAPKYDFPAIQWMETQNTGTNLFDQAFSESVIDSFDFDNPTKPEWYCIEGGTSLLV 312
                                                                                                                               117 ---IPSSHRIVQWFVKKLGVEMNEFVMTDDNTFYLVN-----GVRERTYVVQENPDVLK 167
                                                                                                                                                                                             168 YNVSESEKGISADDLLDRALQKV-----KEEVEANGCKA--ALEKYDRYSVKEYLKEE 218
                                                                                                                                                                                                                                                             G--GLSPG----AVRMIGDLLNEQSLMYTALSEMIYDQADVNDSV--TYHEVTGGSDLLP 270
                                                                                                                                                                                                                                                                                                                             271 EAFLSVLDVPILLNSKVKHIR----QSDKGVIVSYQTGNESSLMDLSADIVLVTTTAKAA 326
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                                      Gaps
                                    88;
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APPLICANT: Greenplate, John T.
APPLICANT: Greenplate, John T.
APPLICANT: Furcell, John P.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: INSECTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALNOID White & Durkee
STREET: HOUSTON
     Length 617;

    Score 417; DB 3; Length 61
    Pred. No. 2.7e-29;
    Mismatches 177; Indels

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ZIP: 77210-4433

MEDIUM RYBE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/09/063,733A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HFAGEHTAFPHAWIETSMKSAIRA 503
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATTEREDON, Welinda L.
REGISTRATION NUMBER: 33,062
     tch 15.4%; al Similarity 31.0%; 156; Conservative 8
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                VVIVGAGMAGLTAAKLLQD----AGHTVTILÄANDRVGGRVET---YRNEKEGWYAEMGAMR
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                   15.4%; Score 417; DB 3; Length 617; 31.0%; Pred. No. 2.7e-29; ive 83; Mismatches 177; Indels
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Patent No. 6248575
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity
TITLE OF INVENTION: NUMBER: US/09/314,242A
CURRENT APPLICATION NUMBER: US/09/314,242A
CURRENT PILING DATE: 1999-05-18
EARLIER PILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 HFAGEHTAFPHAWIETSMKSAIRA 503
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                       TELECOMMUNICATION INFORMATION:
TELEPHORE: 713-797-1440
TELEPAX: 713-797-1440
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acids
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; ORGANISM: Trichoderma harzianum
US-09-314-242-2
                                                                                                                                                                                                                         not relevant
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.0*
Matches 156; Conservative
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. LOCATION: (123) . GOTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-482-273-266
                                                                                                                                                        278 DVPILLNSKVKHI----ROSDKGVI----VSYQTGNESSLMDLSADIVLVTTTAKAALFIDF 331
                                                                                                                                                                                                                                                                                                                                                                                   332 DPPLSISK---MEALRSVHYDSSTKILLTFRDKFWE--DDGIRGGKSIT-DGPS-RYIYY 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 PSHSFHTNETIGVLLASY----TWSDESLLFLGASDEELKELALRDLAKIHGEQ-VWDKC 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 GRVHTEYLSGGPFDYS-----YQEMGPMRFPNTITLGNETYNVSDHQLVFQLAEEMNSL 266
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                                                                                                                             DRALQKVKEEVEANGCKAALEKYDRY--SVKEYLKE------EGGLSPGAVRMIGDL
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APPLICANT: Rosen et al.

TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REPRENCE: P2030P1

CURRENT PILING DATE: 2000-01-13

CURRENT FILING DATE: 1999-07-14

EARLIER APPLICATION NUMBER: PC/1059/15849

EARLIER PILING DATE: 1999-07-15

EARLIER FILING DATE: 1998-07-15

CONTEMN OF DATE: 1998-07-15

CONTEMN OF DATE: 1998-07-15
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, Patent No. 6534631
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SEQ ID NO 266
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Best Local
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14.5%; Score 392; DB 3; Length 695;
Best Local Similarity 27.0%; Pred. No. 6.4e-27;
Matches 148; Conservative 90; Mismatches 195; Indels 1
                        Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regeneral No. 10482).

GENERAL INFORMATION:

APPLICANT: Elizabeth J. Golightly

APPLICANT: Elizabeth J. Golightly

TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides

TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity

FILE REFERENCE: 5556.200-US

CURRENT FELING DATE: 1999-05-18

EARLIER APPLICATION NUMBER: 09/080,428

EARLIER APPLICATION NUMBER: 09/080,428

SEARLIER APPLICATION NUMBER: 09/080,428

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 100
                      14.9%; Score 404; DB 3; Lo
30.6%; Pred. No. 4.2e-28;
ive 84; Mismatches 178;
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                                                                154; Conservative
                                            Similarity
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                          Query Match
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GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508		ALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN 170
458 ALFTPYQHLEYAQELFSSE		120 VVQXPALWQTEKDDW

Search completed: October 4, 2005, 13:48:06 Job time : 45 secs

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October 4, 2005, 13:40:50 ; Search time 479 Seconds (without alignments) 1277.735 Million cell updates/sec
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2703
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1: /cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

2: /cgn2 6/ptodata/1/paa/USOG_COMB.pep:*

4: /cgn2 6/ptodata/1/paa/USOB_COMB.pep:*

4: /cgn2 6/ptodata/1/paa/USOB_COMB.pep:*

5: /cgn2 6/ptodata/1/paa/USOB2_COMB.pep:*

6: /cgn2 6/ptodata/1/paa/USOB2_COMB.pep:*

7: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

9: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

10: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

11: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

12: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

13: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

14: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

15: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

16: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

17: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

18: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

19: /cgn2 6/ptodata/1/paa/USOB3_COMB.pep:*

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14: /cgn2 6/ptodata/1/paa/USOB5_COMB.pep:*

15: /cgn2 6/ptodata/1/paa/USOB5_COMB.pep:*

16: /cgn2 6/ptodata/1/paa/USOB5_COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	E OF INVI	ENTION:	APAPT	SISO	AND ANTICANCER AGENTS			
	REFERENC	CE: 470	3/0F214		770/01/			
	ENT FILL	AG DATE	2003	96	10/044,14			
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Sequence 1, Application US/10645094

GENERAL INFORMATION:
TITLE OF INVENTION: OWEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING
TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS

FILE REPERENCE: 4703/0F214

CURRENT APPLICATION NUMBER: US/10/645,094

CURRENT APPLICATION NUMBER: US/09/912,176

PRIOR PELING DATE: 2001-07-24

PRIOR PELING DATE: 1999-01-22

PRIOR PELING DATE: 1999-01-22

PRIOR PELING DATE: 1999-01-22

PRIOR APPLICATION NUMBER: PCT/JP98/02261

PRIOR APPLICATION NUMBER: PCT/JP98/02261

PRIOR SEQ ID NOS: 2

SOFTWARE: PATENTING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 2

SEG ID NO 1.

TEMMONT. P. 1.
    HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSS
                                                                                          HRIVOWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISAD
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100.0%; Pred. No. 1.1e-246;
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; ORGANISM: Scomber japonicus
US-10-645-094-1
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Sequence 1, Application US/10644142A;
GENERAL INFORMATION:
APPLICANT: Iwamorco, Mitsunori; Jung, Sang-Kee
APPLICANT: Iwamorco, Mitsunori; Jung, Sang-Kee
TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS
TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
CURRENT REPRESENCE: 4703/0F214
CURRENT RELING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1999-05-22
WUMBER OF SEQ ID NOS: 2
SOFUMARE: PARCHIN Ver. 2.0
SSEQ ID NO 1

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Sequence 131193, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bloomix. Inc.
APPLICANT: Bloomix. Inc.
APPLICANT: Bloomix. Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 13193
                      390 HTNETIGVILASYTWSDESLLFLGASDEELKELALRDLAKIH---GEQVWDKCTGVIVKK 446
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                                                            WSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMKSAIRAATN
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44.0%; Pred. No. 1.4e-90;
iive 94; Mismatches 171; Indels
                                                                                                                  507 INKVANEESTIEHTKD 522
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498 VNRASENPSGIHLSND
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Best Local Similarity 44.0%
Matches 218; Conservative
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US-09-791-537-131193
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
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APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: US/09/191,537
CURRENT APPLICATION UNDBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEG ID NO 143961
LENGTH: 516
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                                                       TALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVS
                                                                       33 LADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTILEAND
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44.0%; Pred. No. 6e-91;
ive 96; Mismatches 169; Indels
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Best Local Similarity 44.0%
Matches 218; Conservative
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US-09-791-537-143961
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86 TILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSHRIVQWFVKKLGVEMNEFVMTDDNT 145
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                                                                                                                                                                                                                                         DB 24;
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Pred. No. 5.3e-88;
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TITLE OF INVENTION: Human Secreted Proteins
FILE REPERENCE: PS904PCT
CURRENT APPLICATION NUMBER: PCT/US02/08123
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR PILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
NUMBER OF SEQ ID NOS: 2048
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227,818
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
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Best Local Similarity
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PCT-US02-08123-1068
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ORGANISM: Homo
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US-09-938-795A-1
                                                                                                                                    LENGTH: 630
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 143903
LENGTH: 630
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GENERAL INFORMATION:
APPLICANT: CHU, CHARLES CHIYUAN
APPLICANT: CHU, CHARLES CHIYUAN
APPLICANT: CHAVAN, SANGBETA S.
APPLICANT: MASON, JAMES M.
TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN
FILE REFERENCE: LIJ-9000-US
CURRENT APPLICATION NUMBER: US/09/938,795A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.3%; Score 1034; DB 22; Length Best Local Similarity 43.5%; Pred. No. 5.3e-88; Matches 212; Conservative 100; Mismatches 163; Indels
                                                       S-09-791-537-143903
Sequence 143303, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
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ORGANISM: Mus musculus
US-09-791-537-143903
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US-09-938-795A-1
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Sequence 590, Application PC/TUS0209785
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TILE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS905PCT
CURRENT APPLICATION NUMBER: PCT/US02/09785
CURRENT APPLICATION NUMBER: PCT/US02/09785
CURRENT FILING DATE: 2002-03-19
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEO ID NOS: 1130
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Matches 217; Conservative
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PCT-US02-09785-590
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                                                                                                                                                                                                                              122 RIVOMFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD 181
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                                                                 99; Mismatches 171; Indels
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                                37.0%; Score 999; DB 1;
41.8%; Pred. No. 9.3e-85;
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; Sequence 1025, Application PC/TUS0208278
; GENERAL INFORMATION:
    APPLICANT: Human Genome Sciences, Inc.
    TITLE OF INVENTION: Human Secreted Proteins
    FILE REFERENCE: PS902PCT
    CURRENT APPLICATION NUMBER: PCT/US02/08278
    CURRENT PILING DATE: 2002-03-19
    PRIOR APPLICATION NUMBER: US 60/331,287
    PRIOR FILING DATE: 2001-11-13
    PRIOR FILING DATE: 2001-07-19
    PRIOR FILING DATE: 2001-07-19
    PRIOR FILING DATE: 2001-07-19
    PRIOR FILING DATE: 2001-07-19
    PRIOR FILING DATE: 2001-07-19
    PRIOR FILING DATE: 2001-07-19
    PRIOR PILING DATE: 2001-07-19
    PRIOR FILING DATE: 2001-07-19
    SEQ ID NOS: 1988
    SOFTWARE: PARCENTIN Ver. 2.0
    SEQ ID NOS: 1988
                                               Best Local Similarity 41.89
Matches 217; Conservative
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Best Local Similarity 41.8
Matches 217; Conservative
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ORGANISM: Homo sapiens
PCT-US02-08123-1068
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                                  Query Match
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ETSPPARNLKVLKADVVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRR 361
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                                                                                                   RIVOWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD
VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH
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41.8%; Pred. No. 9.3e-85;
cive 99; Mismatches 171;
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FILING DATE: September 18, 2000
APPLICATION NUMBER: PCT/US00/23522
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Gurney, Austin L
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                                                                                     SFAEALRAHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI 301
                                                                                                                                    QTGNES-SLMDLSADIVLVTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
TITLE OF INVENTION: RELATED DISEASES
TITLE REFERENCE: P1973R1-PCT
CURRENT APPLICATION NUMBER: PCT/US03/21083
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US 60/394,485
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.larity 41.8%; Pred. No. 9.3e-85;
Conservative 99; Mismatches 171
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JILL SCHOENFELD
WILLIAM WOOD
THOMAS WU
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HILARY CLARK
KATHRYN DENNIS
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SEQ ID NO 4
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Best Local Similarity
Matches 217; Conserv
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CURRENT FILING DATE: 2001-06-14
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APPLICATION NUMBER: PCT/US00/32678
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PRIOR APPLICATION NUMBER: 60/113,296
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR APPLICATION NUMBER: 60/107,783
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR FILING DATE: November 10, 1998
PRIOR FILING DATE: November 10, 1998
PRIOR PELICATION NUMBER: 60/084,414
PRIOR APPLICATION NUMBER: 60/084,414
PRIOR APPLICATION NUMBER: 60/085,500
PRIOR FILING DATE: April 23, 1998
PRIOR PILING DATE: April 23, 1998
PRIOR PELING DATE: April 23, 1998
PRIOR PELING DATE: April 29, 1998
PRIOR PELING DATE: April 29, 1998
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/066,772
PRIOR APPLICATION NUMBER: 60/066,772
PRIOR APPLICATION NUMBER: 60/066,772
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 12, 1996
PRIOR PELING DATE: December 12, 1996
PRIOR FILING DATE: December 12, 1996
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PRIOR FILING DATE: December 12, 1996
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PRIOR FILING DATE: December 12, 1996
PRIOR FILING DATE: NOVEMBER: 60/062,702
PRIOR FILING DATE: NOVEMBER: 09/664,610
PRIOR PELING DATE: SEPTEMBER 18, 2000
PRIOR FILING DATE: SEPTEMBER 18, 2000
PRIOR FILING DATE: SEPTEMBER 18, 2000
PRIOR FILING DATE: SEPTEMBER 18, 2000
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FILING DATE: September 18, 2000
APPLICATION NUMBER: 09/665,350
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PILING DATE: February 18, 2000
APPLICATION NUMBER: 09/480,284
FILING DATE: January 10, 2000
TILING DATE: January 10, 2000
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: 09/40,297
FILING DATE: October 18, 1999
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/20111
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APPLICATION NUMBER: 09/423,844
FILING DATE: November 12, 1999
FILING DATE: November 12, 1999
APPLICATION NUMBER: PCT/US99/28301
APPLICATION NUMBER: PCT/US99/28409
                                           FILING DATE: May 30, 2000
APPLICATION NUMBER: PCT/US00/13705
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APPLICATION NUMBER: PCT/USO0/04342
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LICATION NUMBER: PCT/US00/04341
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PPLICATION NUMBER: PCT/0598/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: 09/065,275
  FILING DATE: August 23, 2000
APPLICATION NUMBER: PCT/US00/14941
                                                                                          FILING DATE: May 17, 2000
APPLICATION NUMBER: PCT/US00/08439
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PPLICATION NUMBER: PCT/USO0/05841
PILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/USO0/05004
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APPLICATION NUMBER: PCT/US00/04414
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PPELICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: PCT/US97/22278
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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APPLICATION NUMBER: 09/380,13
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FILING DATE: August
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GENERAL INFORMATION:
APPLICANT: CHU, CHARLES CHIYUAN
APPLICANT: CHARLES CHIYUAN
APPLICANT: CHARLES CHIYUAN
APPLICANT: MASON, JAMES M.
TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN
FILE REFERENCE: LIJ-9000-US
CURRENT APPLICATION NUMBER: US/09/938,795A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-25 IndelB -----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508 37.0%; Score 999; DB 23; 41.8%; Pred. No. 9.3e-85; tive 99; Mismatches 171; Query Match
Best Local Similarity 41.8
Matches 217; Conservative NUMBER OF SEQ ID NOS: 113
SEQ ID NO 13
LENGTH: 567
TYPE: PRT
ORGANISM: Homo Sapien NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin Ver. 3 SEQ ID NO 2 LENGTH: 567 ; ORGANISM: Homo sapiens US-09-938-795A-2 US-09-882-636-13 US-09-938-795A-2 242 421 9 62 122 302 477 TYPE: PRT ઠે 셤 ò g ò 유 à 셤 8 ò g g ઠે g 셤 8 ò ò

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                                              61
                           6 LHL----LVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQR
                                                                                        62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH
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TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR PELING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
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Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
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APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
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Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
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Tumas, Daniel
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Hillan, Kenneth
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R FILING DATE: 1998-09-02
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R APPLICATION NUMBER: 60/098843
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APPLICATION NUMBER: 60/101279
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FILING DATE: 1998-09-17
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FILING DATE: 1998-09-17
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FILING DATE: 1998-09-16
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FILING DATE: 1998-09-16
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R FILING DATE: 1998-09-30
R APPLICATION NUMBER: 60/102487
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APPLICATION NUMBER: 60/101472
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APPLICATION NUMBER: 60/101475
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APPLICATION NUMBER: 60/101915
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APPLICATION NUMBER: 60/102965
FILING DATE: 1998-10-02
APPLICATION NUMBER: 60/103258
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APPLICATION NUMBER: 60/103679
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APPLICATION NUMBER: 60/101916
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APPLICATION NUMBER: 60/102240
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APPLICATION NUMBER: 60/102484
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APPLICATION NUMBER: 60/102687
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APPLICATION NUMBER: 60/103314
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APPLICATION NUMBER: 60/103328
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APPLICATION NUMBER: 60/103395
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APPLICATION NUMBER: 60/103396
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R APPLICATION NUMBER: 60/104987
R FILING DATE: 1998-10-20
R APPLICATION NUMBER: 60/105000
R FILING DATE: 1998-10-20
R APPLICATION NUMBER: 60/105002
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R APPLICATION NUMBER: 60/105693
R FILING DATE: 1998-10-26
A PPLICATION NUMBER: 60/105694
R FILING DATE: 1998-10-26
R APPLICATION NUMBER: 60/105807 Sequence 24, Application US/10001054
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Gorney, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Hebert, Carolyn
APPLICANT: Kabakoff, Rhona APPLICATION NUMBER: 60/105169 FILING DATE: 1998-10-22 APPLICATION NUMBER: 60/105266 FILING DATE: 1998-10-27 Best Local Similarity 41.8 Matches 217; Conservative RESULT 15 US-10-001-054-24 122 182 182 242 302 361 421 242 302 477 467 Query Match PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR ઠે 엄 ò g ò 셤 ò g ò 셤 ઠે d ò 셤 ò g d ò

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FILING DATE: 1999-09-08
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R FILING DATE: 2001-03-09
R APPLICATION NUMBER: 09/866034
R FILING DATE: 2001-05-25
R FILING DATE: 2001-06-01
R APPLICATION NUMBER: 09/892636
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FILING DATE: 2001-07-30
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FILING DATE: 2001-08-06
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APPLICATION NUMBER: 09/423741
FILING DATE: 1999-11-10
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APPLICATION NUMBER: 09/929404
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APPLICATION NUMBER: 09/802706
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               APPLICANT: Watanabe, Colin
APPLICANT: Wacod, William
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: CELL GROWTH
FILE REFERENCE: P30.34TPCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                          PRIOR FILING DATE: 1997-09-17
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FILING DATE: 2000-06-05
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FILING DATE: 2000-09-15
Smith, Victoria
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PRIOR FILING DATE: 2000-03-15
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Best Local Similarity 41.8
Matches 217; Conservative
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ORGANISM: Homo Sapien
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100.0%; Pred. No. 1.3e-216;
tive 0; Mismatches 0; Indels
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Sequence 1, Application US/09912176

Pacent No. US20020034804A1

GENERAL INFORMATION:

APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS

TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS

FILE REFERENCE: 4703/0F214

CURRENT APPLICATION NUMBER: US/09/912,176

CURRENT FILING DATE: 2001/07/24

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-05-22

NUMBER OF SEQ ID NOS: 2

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SONTWARE: PRIOR FLING DATE: 1998-05-22
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US-10-1476-476
US-10-146-476
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ORGANISM: Scomber japonicus
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Best Local Similarity 100.
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Sequence 1,
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3: \cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-938-795A-2

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US-10-121-049-476
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WS-10-645-094-1

Sequence 1, Application US/10645094

Publication No. US20050191737A1

GENERAL INFORMATION:

APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS

FILE REFERENCE: 4703/0F214

CURRENT APPLICATION NUMBER: US/10/645,094

CURRENT PILING DATE: 2003-08-21

PRIOR FILING DATE: 1999-01-24

PRIOR FILING DATE: 1999-01-24

PRIOR PELICATION NUMBER: US/09/120,176

PRIOR FILING DATE: 1999-01-24

PRIOR FILING DATE: 1999-01-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATENTIN VOINGER: PCT/JP98/02261

WUMBER OF SEQ ID NOS: 2

SEG ID NOS: 2

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Publication No. US20040054147A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
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TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
TITLE OF INVENTION UNMBER: US/09/230,388
PRIOR PELLING DATE: 1999-05-22
PRIOR PILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTI OF VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 ELALRDLAKIHG----EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                  Sequence 2, Application US/09938795A

Sequence 2, Application US/09938795A

Publication No. US20030045688A1

GENERAL INFORMATION:

APPLICANT: CHAVAN, SANGETA S.

TITLE OF INVENTION: HUMAN INTERLUKIN-FOUR INDUCED PROTEIN

FILE REFERENCE: LIJ-9000-US

CURRENT APPLICATION NUMBER: US/09/938,795A

CURRENT APPLICATION NUMBER: 05/09/938,795A

CURRENT PILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-08-25

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 567;
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US-09-946-374-84
IS-09-946-374-84
; Sequence 84, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
    508
  502 RAATNIN
                                        RAAVRIN
                                                                                                         RESULT 5
US-09-938-795A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 TILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSHRIVQWFVKKLGVEMNEFVMTDDNT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 FYLVNGVRERTYVVQENPDVLKYNVSESEKGISADDLLDRALQKVKEEVEANGCKAALEK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 YDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVTGG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 SDILLPEAFLSVLDVPILLINSKVKHIRQSDKGVIVSYQTGNESSLMDLSADIVLVTTTAKA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 WDLLPRALLSSLSGALLLNAPVVSITQGRNDVRVHIATSLHSB-KTLTADVVLLTASGPA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 ALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIRGGKSITDGPSRYIYYP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIHGE---OVWDKCTGV 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443 IVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE-GRVHFAGEHTAFPHAWIETSMKSAI 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AASSLNPIEKCMEDHDYEQLLKVVTLGLNRTSKPQKVVVVGAGVAGLVAAKMLSDAGHKV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFWEDDGIRGGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 ALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 ARGEGS----LLLASYTWSDAAAPFAGLSTDQTLRLVLQDVAALHGPVVFRLWDG-RGV
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                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09938795A
Publication No. US200300456881
GENERAL INFORMATION:
APPLICANT: CHU, CHARLES CHIYUAN
APPLICANT: CHAVAN, SANGEETA S.
APPLICANT: MASSON, JAMES M.
TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN
FILE REFERENCE: LIJ-9000-US
CURRENT APPLICATION NUMBER: US/09/938,795A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO.
                                                                                                                                                                                                            481 FAGEHTAFPHAWIETSMKSAIRAATNINKVANEESTIEHTKDEL 524
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                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-938-795A-1
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R APPLICATION NUMBER: 60/100627
R FILING DATE: 1998-09-16
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APPLICATION NUMBER: 60/102487
FILING DATE: 1998-09-30
APPLICATION NUMBER: 60/102570
FILING DATE: 1998-09-30
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FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100683
FILING DATE: 1998-09-17
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FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/100711
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APPLICATION NUMBER: 60/100848
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FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/100930
FILING DATE: 1998-09-17
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FILING DATE: 1998-09-23
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FILING DATE: 1998-09-23
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FILING DATE: 1998-09-23
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APPLICATION NUMBER: 60/101479
FILING DATE: 1998-09-23
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FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/101916
FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/102240
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FILING DATE: 1998-09-29
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FILING DATE: 1998-09-18
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APPLICATION NUMBER: 60/101071
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FILING DATE: 1998-09-23
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FILING DATE: 1998-09-24
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FILING DATE: 1998-09-24
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FILING DATE: 1998-09-29
                                                                                                                                                                                                            APPLICATION NUMBER: 60/100684
FILING DATE: 1998-09-17
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FILING DATE: 1998-09-29
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FILING DATE: 1998-09-16
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-09-04

PRIOR APPLICATION NUMBER: 60/098716

PRIOR FILING DATE: 1998-09-01

PRIOR FILING DATE: 1998-09-01

PRIOR FILING DATE: 1998-09-01

PRIOR FILING DATE: 1998-09-01

PRIOR PLING DATE: 1998-09-01

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PRIOR PLING DATE: 1998-09-02

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Grimaldi, Christopher J.
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APPLICATION NUMBER: 60/100584
                                                                                                                                                                                                                                            Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
                                                                       Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                           Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                      Gurney, Austin L.
Hillan, Kenneth J
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                                   Desnoyers, Luc
Eaton, Dan L.
Baker, Kevin P.
                                                                                                                                                                                                                                Pan, James
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362 PFWREEHIEGGHSNTDRPSRMIFYP-----PPREGALLLASYTWSDAAAAFAGLSREEAL 416
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                                                                                                                                                                                                                                                                                                                                                                                       417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQGGFVVQPP-----ALWQTEK 466
242 SFAEALRAHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WOOSL, MILLIAM
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
CURRENT FILING DATE: 1097-00-17
PRIOR PELLING DATE: 1097-00-17
PRIOR FILING DATE: 1098-00-30
PRIOR PELLING DATE: 1098-00-30
PRIOR PELLING DATE: 1098-00-30
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Publication No. US20020192209A1
GENERAL INFORMATION:
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Goddard, Audrey
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Hebert, Carolyn
Kabakoff, Rhona
Shalton, David
Smith, Victoria
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                                    PRIOR FILLING DATE: 1998-10-30
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APPLICANT: Goddward, Audrey
APPLICANT: Goddward, August 1.
APPLICANT: Goddward, August 1.
APPLICANT: Gordward, August 1.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune IIIE REPERENCE: 13033R1C1
CURRENT APPLICATION NUMBER: US/10/053,107
CURRENT FILING DATE: 2002-01-17
CURRENT FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/107783
PRIOR PILING DATE: 1998-11-17
PRIOR PILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/113296
PRIOR PILING DATE: 1999-04-27
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41.8%; Pred. No. 2.8e-74;
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Publication No. US20020192752A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/232897
PRIOR FILING DATE: 2000-09-15
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NUMBER OF SEQ ID NOS: 14
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Matches 217; Conservative
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; ORGANISM: Homo Sapien
US-10-053-107-2
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R FILING DATE: 1997-10-28

R APPLICATION NUMBER: 60/063561

RR APPLICATION NUMBER: 60/063704

RR APPLICATION NUMBER: 60/063704

RR APPLICATION NUMBER: 60/063704

RR APPLICATION NUMBER: 60/063733

RR APPLICATION NUMBER: 60/063735

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RR FILING DATE: 1997-10-29
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R FILING DATE: 1997-11-07
R APPLICATION NUMBER: 60/065186
R FILING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065846
R FILING DATE: 1997-11-17
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RR FILING DATE: 1998-01-23
R PFLING DATE: 1998-02-04
RR FILING DATE: 1998-02-04
RR PILING DATE: 1998-02-09
RR FILING DATE: 1998-02-09
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FILING DATE: 1998-02-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081695
             FILING DATE: 1997-10-27
APPLICATION NUMBER: 60/063329
FILING DATE: 1997-10-27
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066511
FILING DATE: 1997-11-24
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APPLICATION NUMBER: 60/069378
APPLICATION NUMBER: 60/069334
FILING DATE: 1997-12-11
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082999
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FILING DATE: 1997-10-17
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FILING DATE: 1997-11-03
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FILING DATE: 1997-11-21
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FILING DATE: 1997-12-16
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FILING DATE: 1998-03-25
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/063327
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421 ELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
                        ---ALWQTEK 466
              477 -----GRVHFAGEHTAFPHAWIETSMKSAIRAATNIN 508
                                                               467 DDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505
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Publication No. US20030004311A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/063127
FILING DATE: 1997-10-24
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Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Wood, William
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DeForge, Laura
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Filvaroff, Ellen
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ITLE OF INVENTION:
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US-10-028-072-476
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362 PFWREBHIEGGHSNTDRPSRMIFYP-----PPREGALLLASYTWSDAAAAFAGLSREEAL 416
                                        242 SFAEALRAHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQI 301
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          VVIVGAGMAGLTAAKLLODAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSH
                                                                                                                                                                                                       182 LLDRALOKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMYT
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumash, Daniel
APPLICANT: Tumash, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
                                                                                                        RIVOMFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD
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41.8%; Pred. No. 2.8e-74;
tive 99; Mismatches 171;
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Desnoyers, Luc
Filvaroff, Bllen
Gao, Wei-Qiang
Gertitsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Best Local Similarity 41.9
Matches 217; Conservative
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US-10-140-808-476
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                 PRIOR APPLICATION NUMBER: 60/084545
PRIOR FILING DATE: 1998-04-28
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
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R APPLICATION NUMBER: 60/083322
R FILING DATE: 1998-04-28
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/084500
R APPLICATION NUMBER: 60/084600
R APPLICATION NUMBER: 60/084627
R APPLICATION NUMBER: 60/084627
R FILING DATE: 1998-05-07
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Indels

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41.8%; Pred. No. 2.8e-74; ive 99; Mismatches 171;
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Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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al Similarity 41.8% 217; Conservative
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Filvaroff, Ellen
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT APPLICATION NUMBER: US/202-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 567
TYPE: PRT
                                                                                                                                    LHVVKWKLSVVSVLITLYYSHT-VALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHH
                        LHL----LVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQR
                                                         12 RIVOWFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADD
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Publication No. US20030022239A1
GENERAL INFORMATION:
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Gerritsen, Mary E.
Goddard, Audrey
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333OHER: US/10/123,904
CURRENT APPLICATION NUMBER: 2002-04-16
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32;
  Indels
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ORGANISM: Homo Sapien
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US-10-175-746-476
    LENGTH: 567
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OP INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OP INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
                                                         32;
                             Length 567;
                                                        99; Mismatches 171; Indels
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                          37.0%; Score 999; DB 14;
41.8%; Pred. No. 2.8e-74;
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Publication No. US20030022331A1
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Filvaroff, Ellen
Gao, Wei-Oiang
Gerriteen, Mary
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Wood, William
                                         Best Local Similarity 41.89
Matches 217; Conservative
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US-10-123-904-476
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R12353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
                                                                                               Length 567;
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                                                                                           ; Score 999; DB 14;
; Pred. No. 2.8e-74;
99; Mismatches 171;
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41.8%;
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Smith, Victoria
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Filvaroff, Ellen
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-476
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Best Local Similarity
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GENERAL INFORMATION:

APPLICANT: Beresini, Maureen
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APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wet-Qiang
APPLICANT: Gao, Wet-Qiang
APPLICANT: Godwski, Paul J.
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APPLICANT: Smith, Victoria
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APPLICANT: Timochy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
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APPLICANT: ANOCA, William
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                                                                                                                                                                                                   37.0%; Score 999; DB 14; Length 567; 41.8%; Pred. No. 2.8e-74; Live 99; Mismatches 171; Indels 33
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  or
Wrapper
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Publication No. US20030027275A1
GENERAL INFORMATION:
- See File
                                                                                                                                                                                                                                   al Similarity 41.8
217; Conservative
Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 476
                                                                                                       TYPE: PRT
CORGANISM: Homo Sapien
US-10-175-746-476
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Best Local Si
Matches 217;
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CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 550
SEQ ID NO 476
LENGTH: 567
                                                                                                                                                                                                                    Ouery Match
37.0%; Score 999; DB 14;
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171;
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Oct

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5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2005 Copyright

sw model - protein search, using OM protein 4, 2005, 13:48:15; October Run on:

; Search time 43 Seconds (without alignments) 1172.502 Million cell updates/sec

score:

US-10-645-094-1 2703 1 MNLHVVVKWKLSVVSVLITLY.....TNINKVANEESTIEHTKDEL Perfect sc Sequence:

524

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 200000000 08 08 Minimum

Post-processing: Махітит

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR 79:* 4 3 2 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

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828260	T21327 I39708	T47787	T09935	S54021	A47259	T26783	A84861	T33175	T39423	S55273	T24218	F71403	A39597	S16250
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240.5	231.5	225.5	224.5	220.5	216	209.5	205	198.5	198.5	186	186	184	184	183.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

L-amino-acid oxidase (EC 1.4.3.2) - eastern diamondback rattlesnake
N.Alternate names: LAAO; ophio-amino-acid oxidase
C;Species: Crotalus adamanteus (eastern diamondback rattlesnake)
C;Species: Crotalus adamanteus (eastern diamondback rattlesnake)
C;Accession: JE0266
R;Raibekas, A.A.; Massey, V.
B;C;Accession: JE0266
R;Raibekas, A.A.; Massey, V.
A;Title: Primary structure of the snake venom L-amino acid oxidase shows high homology A;Reference number: JE0266; MuID:98369573; PMID:9703950

A;Molecule type: mRNA A;Residues: 1-516 cRAL> A;Cross-references: UNIPROT:093364; GB:AF071564; NID:g3426323; PIDN:AAC32267.1; PID:g342 C;Keywords: oxidoreductase

Gaps 13; Length 516; 94; Mismatches 171; Indels Score 1059.5; DB 2; Pred. No. 1.1e-60; 39.2%; Matches 218; Conservative Query Match Best Local Similarity

LADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTILEAND

ò g ò

212 85 g ò

RERTYWYGENPDVLKYNVSESEKGISADDLLDRALQKVKEEVEANGCKAALEKYDRYSVK 153 g

EYLKEEGGLSPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVTGGSDLLPEA 213 203 à ద

273 FLSVL--DVPILLNSKVKHIRQSDKGVIVSYQT-GNESSLMDLSADIVLVTTTAKAALFI 329 320 263 ò 요

DEDPPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIRGGKSITDGPSRYIYYPSHSF 389 330 321 ò g

δ g

WSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMKSAIRAATN 506 438 447 ò 유 N

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Cybace: 10. bulled-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cybace: 0. bulled-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
CyAccession: E69899
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosnon, S.; Hullo, M.F.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Darro, V.; Poll, T.M.; Portecelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Schowska, A.; Terpstra, P.; Togato, V.; Poll, T.M.; Portecelle, R; Record, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamancho, H.; Yamancho, H.; Yasamancho, H.; Yasamancho, H.; Yasamancho, V.; Vata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Residues: 1-446 cKUN>
A; Residues: UNIPROT:034363; GB:299114; GB:AL009126; NID:g2634230; PIDN:CAB13794.
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: Laninary: A; Genetics: Rrain 168
C; Genetics:
A; Genetics: Rrain 168
C; Genetics: A; Genetics: Rrain 168
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C;Date: 09-May-2004 #sequence_revision 09-May-2004 #text_change 09-May-2004
C;Accession: JC8062
R;Arime, T Tamura, T., Kusakabe, H., Ashiuchi, M., Yagi, T., Tanaka, H., and Inagaki, J. Biochem. 134, 805-812, 2003
A;Title: Recombinant expression, biochemical characterization and stabilization through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IKKFKLPTNVFINRTPMDIIYANGIKTRLQVPERAPGILRYPVAPNEQGKTSEELMLSLL
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36.4%; Pred. No. 5.3e-40;
ive 89; Mismatches 187;
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GEHASLTHAWMQGAIESGIRVAYEVNRL 445
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Matches 163; Conservative
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                                                                                                                                                                                                                                Leanino-acid oxidase (EC 1.4.3.2) precursor, TSV-LAO - Chinese green tree viper U. Alternate names: ophio-amino-acid oxidase (Specias: Trimeresurus stepinegeri (Chinese green tree viper)

C.Specias: Trimeresurus stepinegeri (Chinese green tree viper)

C.Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004

C.Accession: JC8015

R.Zhang, Y.J.; Wang, J.H.; Lee, W.H.; Wang, Q.; Liu, H.; Zheng, Y.T.; Zhang, Y.
Biochem. Biophys. Res. Commun. 309, 598-604, 2003

A;Title: Molecular characterization of Trimeresurus stejnegeri venom L-amino-acid oxidas

A;Reference number: JC8015; PMID: 12963032

A;Residues: 1-516 < ZHA>

A;Residues: 1-516 < ZHA>

A;Residues: 1-516 < ZHA>

A;Cross-references: GB:AY277739

A;Experimental source: Venom

C;Comment: This enzyme is a flavo-enzyme which catalyzes the stereospecific oxidative de peroxide (H2O2): TSV-LAO enzyme from venom is a homodimeric, FAD-binding glycoprotein wi C;Genetics:

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Keywords: antiviral activity; glycoprotein; L-amino-acid oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.0%; Score 1055.5; DB 2; Length 516; 42.8%; Pred. No. 2.1e-60;
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C;Species: Bacillus subtilis
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Best Local Similarity
Matches 212; Conserv
                                                                                    498
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A;Title: Genome sequence of the radioresistant bacterium A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                          A;Cross-references: UNIPROT: O9RYN6;
A;Experimental source: strain R1
C;Genetics:
                                A,Accession: A75581
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-526 <WHI>
                                                                                                                                                           N
                                                                                                                                           A;Gene: DRA0274
A;Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: alr7169
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A, Reference number: JC8062, PMID: 14769868
A; Accession: JC8062
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-701 <ARI>
A; Residues: 1-701 <ARI>
A; Experimental source: (Strain x-119-6)
C; Comment: This enzyme precursor is a protein of 150K with hexamer structure alpha2-beta no non-covalently bound FAD as a coffactor. It catalyzes the oxidative deamination of an in quantitative assaying of L-glutamate existing in food and in a fermentation process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flavin monoamine oxidase-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Daccession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75581
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamatheyan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          KSFKDGKTWTNGAPSPEFKEPDKRNHTWIRTNREQVRRAQYATDPSSINEGFHLTGCETR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 LTVSDMVNQALEPVRDYYSVKQDDGTRVNKPFKEWLAGWADVVRDFDGYSMGRFLREYAE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSPGAVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVTYHEVTGGSDLLPEAFLSVLDVP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 FSDEAVEAIGTIENMTSRLHLAFFHSFLGRSDIDPRATYWEIEGGSRMLPETLAKDLRDQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527
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                                                                                                                                                                                                                                                                                   49 LDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTILEAN-DRVGGRVETYRNEK--
                                                                                                                                                                                                                                                                                                                                                                  108 PSPFADPAQYAEAGAMKLPSFHPLTLALIDKLGLKRRLFFNVDIDPOTGNODAPVPPVFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISADDLLDRALQKVKEEVEAN-------GCKAALEKYDRYSVKEYLKEEGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 ---GGKSITDGPSRYIYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528 NAYGGGSTIDNPNRFMYYPSHPVPGTQG-GVVLAAYSWSDDAARWDSFDDAERYGYALEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYQQWGEDDAEAALALPQSVRNLPTGLLGAHPSVDESRIGEEQVEYYRNSELRGGVRPAT
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                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                      164;
                                                                                                                                                                                                                       Length 701;
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                                                                                                                                                                                                                     Query Match
23.7%; Score 641; DB 2; Length 70
Best Local Similarity 27.2%; Pred. No. 1.8e-33;
Matches 170; Conservative 95; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 KAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFW----
                                                                                                                                                        ;Gene: Lgox
;Start codon: GTG
;Keywords: hexamer structure; L-glutamate oxidase
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L-amino acid oxidase [imported] - Nostoc sp. (strain PCC 7120) plasmid pcC7120alpha L-amino acid oxidase [imported] - Nostoc sp. (strain PCC 7120 A;Note: Nostoc sp. PCC 7120 C;Space: Solution of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Uul-2004 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Uul-2004 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Uul-2004 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Uul-2004 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takázawa, M.; Yamada, M.; Yasuda, M.; Tabata, E DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Residues: 1-445 eKURA
A;Residues: 1-445 eKURA
A;Cassa: references: UNIPROT:QBYKW9; GB:BA000020; PIDN:BAB78253.1; PID:g17135707; GSPDB:CASSPERIEMENTAL SOURCE: strain PCC 7120
A;Experimental source: strain PCC 7120
A;Ganetics:
                                                                                                                                                                                   GB:AE001825; NID:g6460670; PIDN:AAF124
RI.
radiodurans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SVKEYLKEEGG-LSPGA-VRMIG-DLLNEQSLMYTALSEMIYDQADVNDSVTYH---
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
      Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                               90;
                                                                                                                                                                                                                                                                                                                                                             Query Match
15.2%; Score 412; DB 2; Length 526;
Best Local Similarity 27.5%; Pred. No. 6.7e-19;
Matches 140; Conservative 86; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKE
                                                                                                                                                                                      GB:AE001863;
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TSYWNGWQEGALLAATTAVQEMHKFASSQA 526
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amine oxidase, flavin-containing [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87595
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87595
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: UNIPROT:09A4N7; GB:AE005673; NID:g13424393; PIDN:AAK24757.1; GSPDB:G.
C;Genetics:
A;Gene: CC2793
                                                                                                                                                                                                                                                                                                   331
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--ALTRVSN----NSTKSLSQKVDAFLPDTDKFLAEMAQNMFKAHADWLSGGLAGLPGDQ 368
                                                                                                                                                                                         --YHEVTGGSDLLPEAFLSVL 277
                                                                                                                                                                                                                                                                                                                                                            484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSHSFHTNETIGVLLASY----TWSDESLLFLGASDEELKELALRDLAKIHGEQ-VWDKC 439
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                                                                                                                                                                                                                                                                                                     DVPILLNSKVKHI----RQSDKGVI---VSYQTGNESSLMDLSADIVLVTTTAKAALFIDF
                                                                                                                                                                                                                                                                                                                                        126 GNYFNPGPWRIPHHRITLLHYCKQFGVALEPFIQFNH-----SGWIHSSQAFGGKP--V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSHRGFKRPGGGGVDGAPIPSDDLYSLHDVLDPQ--VWTSMGFFMNHEM----QTTMFQP
                                                                                  DRALQKVKEEVEANGCKAALEKYDRY - - SVKEYLKE - - - - - - EGGLS PGAVRMIGDL
                                                                                                                                                                                                                                                  WSEFGFMVNYLRGSLNDTAFLAPALTRTGTRCTKGCTFPRRRGAIDGGLNRLPLSFHPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYR-------NEKEGW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYNVSESE-----KGISADDLLDRALQKVKEE-VEANGCKAALEKYDRY-----
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Pred. No. 4.8e-17;
2; Mismatches 209;
                                                                                                                                                                                            LNEQSLMYTALSEMIYDQADVNDSVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.2%; Sccilarity 26.7%; Pre
Conservative 92;
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SGIRGSVQL 670
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                                                                                                                                                                                                                                                                                                        130 KLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADDLLDRALQK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIGDLLNEQSLMYTALSEMIYD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGWGFFDD------EELWHTTWDRPEKTGILHA-YLKGEKGLEIDGFEGKTQQQKLL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q-----HWEKILPGVSNYSVRSYFHSWTKDIWSKGGWAYPTDEQEKKLFPELGKSEGKIY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QADVNDSVTYHEVTGGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSYQTGNESSL 309
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                                                                                                                                                                                                                   16
                                                                                                                                                                                               --YLGDYVLCTVPLTVLNQITFSPELSEEKKQAAAGGYNYRAATRGFVKFPNRFWERENL
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                                                                                                                                                                                                                                                                         GLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGW-YAEMGAMRIPSSHRIVQWFVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGGKSITDGPSRYIYYPSHSFHTN----ETIGVLLASYTWSDESLLFLGASDEELKELAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDLAKIHGEQVWDKCTGVIVK----KWSADPYSLGAFALFTPYQHLEYAQELFSSEGRVH
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                                                                                                               Gaps
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                                                                                                            134;
                                                         Length 426;
                                                                                                            72; Mismatches 172; Indels
                                                      14.5%; Score 392; DB 2; 25.6%; Pred. No. 9.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LL
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FAGEHTSKTRGWLQGALESGLKAAQEIH 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                            HFGLKLSQFAPADGKYLTIKDGKR-
                                                                                                                                                                                                                   35 STLAIAATVSYDHVOAOKPKSP---
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les 148; Conservative
                                                                                                            Conservative
                                                   Query Match
Best Local Similarity
Matches 130; Conserv
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A,Genome: plasmid
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83592
C;Accession: H83592
R;Stover, CK:; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ..., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic paths A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:AE004479; GB:AE004091; NID:g9946272; PIDN:AAG0381
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     RIVOMFVKKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSE---SEKGIS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AD-----DLLDRALQKVKEEVEANGCKAALEKYDRYSVKEYLKEEGGLSPGAVRMIG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRIRSRYDEPSRLSLLYLAQQGRAYRGVDDAD-LRAARLPGGSQVLAEAFVKQIKT-IKT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 KSKVSIVQAKDGVAV--KAGSET----YKADYVVLAVPLKALGQIQMTPSLSGTQMSAL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSVHYDSSTKILLTFRDKFWEDDGIRGGKSITDGPSRYIYY-PSHSPHTNETIGVLLASY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGTNYGWRDO11LLKFKRPVWDDKSRLSGE1PSDOGLGMIWVEPALKGGANVLINLS---- 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWSDESLLFLGASDEELKELALRDLAKIHGEQVWDKCTGVIVKKWSADPYSLGAFALFTP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :: | :: | :: | | :- | :- | :- | -- GDNARVLQAFGDRQWLDQVLIRMNKFY-PXMRGAFAGYEIRRYSADFGTGGSYLAYGP 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOHLEYAQELFSSEGRVHFAGEHT-AFPHAWIETSMKSAIRAATNINKV-ANEESTIE 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tryptophan 2-monooxygenase (EC 1.13.12.3) - Pseudomonas syringae pv. savaste
C;Species: Pseudomonas syringae pv. savastanoi
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25493
R;Yamada, T.; Palm, C.J.; Brooks, B.; Kosuge, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 VIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNEKEGWYAEMGAMRI-PSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYLDTF-KLKPVPAPDFVRTPS---YLIDG------LYYSSSDLALKQPNVA
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                                                                                                                                                                                                                                                               - Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.4%; Score 307; DB 2; L 27.0%; Pred. No. 3.6e-12; ive 83; Mismatches 200;
                                                                                  FAGEHTAFPHAWIETSMKSAIRAATNIN 508
                                                                                                               LAGEHLSYLGGWQAGAIESAWQQIAKIH
                                                                                                                                                                                                                                                             hypothetical protein PA0421 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Accession: H83592
A.Accession: H83592
A.Status: preliminary
A.Kolecule type: DNA
A.Residues: 1-496 <STO>
A.Cross-references: UNIPROT:091692; GB
A.Experimental source: strain PAO1
C.Genetics:
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Matches 129; Conservative
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
R;Mccman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acada Sci. US.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87384
A;Accession: G87384
A;Residues: L-534 <STO>
A;Residues: 1-534 <STO>
A;Crosse-references: UNIPROT:Q9A9A3; GB:AE005673; NID:g13422395; PIDN:AAK23075.1; GSPDB:C
382 IYYPSHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIHGEQVWDKC-T 440
                                                                                                                                                                                                                                                                                  441 GVIVKKWSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMKSA 500
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                                                                          AKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFW-EDDGIRGGKSITDGPSRY 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nine oxidase, flavin-containing [imported] - Caulobacter crescentus Species: Caulobacter crescentus ispecies: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                               48 TLDNGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETYRNE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KEGWYAEMGAMRIPSSHRIVQWFVKKLGVEMNEFVMTDDNTF-YLVNG
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                                                                                                                                                                                                                                                                                                                                                                                     501 IRAATNINKVA 511
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528 LDAITRLHKRA 538
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A; Gene: GDB: MAOB
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Best Local 8
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NyAlternate names: monomine oxidase B
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1933 #sequence revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JH0817; JH0818; E36175; I62455; S66431
R;Chen, K.; Wu, H.F; Shih, J. C.
J. Neurochem. 61, 187-190, 1993
A;Title: The deduced amino acid sequences of human platelet and frontal cortex monoamine
A;Reference number: JH0817; MUDD:93294582; PMID:8515265
A;Accession: JH0817
A;Molecule type: mRNA
A;Residues: 1-520 cMIN
A;Experimental source: platelet
A;Accession: JH0818
A;Accession: JH0818
A;Accession: JH0818
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A;Accession: JH0818
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A;Accession: JH0818
A;Accession: JH0818
A;Cross-references: GB:S62734; NID:g398414; PIDN:AAB27229.1; PID:g398415
A;Cross-references: GB:S62734; NID:g398414; PIDN:AAB27229.1; PID:g398415
                            genes show
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                                                                                                                                                                                                                                                                                                                                                          119 SSHRIVQWFVKKLGVEMNEFV----MTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESE 174
                                                                                                                                                                                                                                                                                                                                                                                           PSATGLFHYLKKFGISTSTTFPDPGVVDTELHY--RGKRYHWPAGKKPPELFRRVYEGWQ 158
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                            acid
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                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 PPGGDRWARPEDFELFGSLGIGS----GGFLPVFQAGFTEILRMVINGYQSD-----
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 82, 6522-6526, 1985 of the Pseudomonas savastanoi indoleacetic
                                                                                                                                                                                                                                                      Indels 106;
                                                                                                                                                                                                                       Length 557;
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                                                                                                                                                                                                                                      / Pred. No. 9e-12;
83; Mismatches 202;
                                                                                                                                      A,Gene: iaaM
C,Superfamily: Pseudomonas tryptophan 2-monooxygenase
C,Keywords: monooxygenase; oxidoreductase
                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 KGISADDLLDRALQKVKEEVEANGCKAALEKY----
                                                                                                                                                                                                                   Score 302;
Pred. No. 9
              A,Title: Nucleotide sequences of the A,Reference number: A94062
A,Accession: A25493
A;Molecule type: DNA
A,Residues: 1-557 < YAM\S
A,Cross-references: UNIPROT:P06617
C,Genetics:
                                                                                                                                                                                                                   11.2%;
24.8%;
Proc. Natl. Acad. Sci. U.S.A. A, Title: Nucleotide sequences A; Reference number: A94062
                                                                                                                                                                                                                                Best Local Similarity 24.89
Matches 129; Conservative
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A; Cross-references: GB:M69135; GB:J03793; NID:g187374; PIDN:AAA59551.1; PID:g187376

A; Cross-references: GB:M69135; GB:J03793; NID:g187374; PIDN:AAA59551.1; PID:g187376

A; Cross-references: GE:M69135; GB:J03793; NID:g187374; PIDN:AAA59551.1; PID:g187376

A; Zhu, Q.S.; Grimsby, J.; Chen, K.; Shih, J.C.

J. Neurosci. 12, 4437-4446; 1992

A; Title: Promoter organization and activity of human monoamine oxidase (MAO) A and B gen:

A; Reference number: 141054; MUID:93057796; PMID:1432104

A; Accession: 162455

A; Accession: 162455

A; Residues: 1-15 and A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A; ARB A
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                                                                  S.W.
                                                                                                                                                   B: molecular basis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 TINGGQERKEVGGSGQVSERIMDLLGDRVKLERPVIYIDQTRENVLV--ETLNHEM---Y 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSYQTGNESSLMDL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                             M.E.; Kwan,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 SITDGPSRYIYY-----PSHSFHTNETIGVLLASYTWSDESLLFLGASDEELKEL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL----TKEERLKKLCELY
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A;Experimental source: cerebral cortex
R;Bach, A; Lan, N.C.; Johnson, D.L.; Abell, C.W.; Bembeng
Broc. Natl. Acad. Sci. U.S.A. 85, 4934-4938, 1988
A;Title: cDNA cloning of human liver monoamine oxidase A and I
A;Reference number: A36175; MUID:88263063; PMID:3387449
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AVRMIGDLLNEQSLMYTALSEMIYDQADVNDSVT--YHEVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 288; DB 2; L, 25.0%; Pred. No. 6.5e-11; Live 84; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:119377; OMIM:309860
A;Map position: Xp11.23-Xp11.23
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: S66431
A, Molecule type: protein
A, Residues: 371-391 < CES>
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Mar

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EMBL: AJ002204; NID: 93043528; PIDN: CAA05249.1; PID: 9
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03387
R;Tavladoraki, P: Schinina, M: Cecconi, F: Di Agostino, S:; Manera, F: Rea, G.; Migral Lett. 426, 62-66, 1998
A;Title: Maize polyamine oxidase: primary structure from protein and cDNA sequencing. A;Reference number: Z14918; MUID: 98258926; PMID: 958979
A;Accession: T03387
A;Accession: T03387
A;Accession: T03387
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-500 < ATAV>
A;Cross-references: UNIPROT: O64411; EMBL: AJ002204; NID: G3043528; PIDN: CAA05249.1; PID
A;Note: flavin-containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.81
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                     A,Gene: PAO
A,Genome: plasmid pCR2.1
C,Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHRIVQWFVKKLGVE-MNEFV---MTDDNTFYLVNGVRERTY--VVQENPDVLKYNVSES 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 SQACLFYLLEYLGINAMTKFFNPGTVDTGLYY----RGRSYNWKAHSLPPAIFNRVHKG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 AHPPGGEKWTRDVDMELFKELGVGSGGFGPVFGCGFIEILRLIVNGYEDNVMLLLDGIEE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 LAIGEG-----MHATFDRVIVTSGFTNIQLRHLLINDDSFFSYDVNQAIENSHMTGSSKL 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EK-----GIS----- GIS----- ADDLLDRALQKVKEEVEANGCKAAL-- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 WRTFLHAGFVDGVAAPASPFILTECLRLRNYEFASSLWQKWLDAFSSETFSSGIERIFRG 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EKYDRYSVKEYLKE----EGGLSP----GAVRMIGDLLN--EQSLMY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 FVLTQNKFWKAEEL-PSCILTTGVAKAVYCLDYEPDKPSGKGLVLLSYTWEDDSHKLLTF
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polyamine oxidase (EC 1.5.3.11) precursor - maize plasmid pCR2.1
C;Species: Zea mays (maize)
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                                                        Indels
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llarity 23.8%; Pred. No. 1.2e-10;
Conservative 83; Mismatches 198;
                           GRVHFAGEHTAFPH--AWIETSMKSAIRAATNI
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Best Local Similarity
Matches 125; Conserv
                           477
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amine oxidase (flavin-containing) (EC 1.4.3.4) A - human
NyAlternate names: adrenalin oxidase A; amine oxidase A; monoamine oxidase A; tyraminase
C;Specasion appiens (man)
C;Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: A36175; JL0066; A28935; 184543; S23360
C;Accession: A36175; JL0066; A28935; 184543; S23360
Proc. Natl. Acad. Sci. U.S.A. 85, 4934-4938, 1988
A;Title: cDNA cloning of human liver monoamine oxidase A and B: molecular basis of diffe
                                                                                                                                                                                                                                                70 AGLTAAKLLQDAGHT-VTILEANDRVGGRVETYRNEKEGWYAEMGAMRIPSSHRIVQWFV 128
                                                                                                                                                                                                                                                                                                                                                                         KKLGVEMNEFVMTDDNTFYLVNGVRERTYVVQENPDVLKYNVSESEKGISADDLLDRALQ 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457
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                                                                                                                                                                                                                                                                                                                                                                                                                      GVNGGGMNPIWPIVNSTLKLRN------PRSDFDYLAQNVYKEDGGVYDEDVVQKRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GSLAATVGPRVIVVGAGM
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                                                                                                                         10 LSVVSVLITLYYSHTVALSLKEHLADCLEDKDYDTLLQTLDNGLPHINTSHHVVIVGAGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVKEEVEANGCKAALEKY - - - DRYSV - - KRYLKEEGGLSPGA - VRMIGD - - - - - -
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                                                                93;
      500;
      Length
                                                                   Indels
10.6%; Score 285.5; DB 2; 25.8%; Pred. No. 8.9e-11;
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Search completed: (
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X;Reywords: dimer; RAD; flavoprotein; mitochondrion; oxidoreductase; phosphoprotein 
F;15-43/Region: beta-alpha-beta FAD nucleotide-binding fold 
F;406/Modified site: S-(8alpha-FAD)-cysteine (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Residues: 1-102;38-527 <CHW>
A/Cross-references: EMBL:X60818
A/Octost the nucleotide sequence was submitted to the EMBL Data Library, July 1991
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
C/Goment: This protein is an integral protein of the outer mitochondrial membrane and C/Genetics:
A/Gene: GDB:WAOA
A/Gene: GDB:WAOA
Cross-references: GDB:120164; OMIM:309850
C/Complex: dimer
C/Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 RILR-LSKELGIETYKVNVSE----RLVQYVKGKTYPFRGAFPPVWNPIAYLDYN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 KGISADDLLDRALQKVKEEVEANGCKAA--LEKYDRYSVKEYLKEEGGLSPGAVRMIGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.5%; Score 283; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.4e-10;
Matches 121; Conservative 91; Mismatches 197; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NLWRTIDNMGKEIPTDAPWEAQHADKWDKWTMKE----
A; Reference number: A36175; MUID: 88263063; PMID: 3387449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 LNEQSLMYTALSEMIYDQADVNDSVTYHEVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::
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Db 161 IDKICWTKTA-RRFAYLFVNINVTSEPHEVSALWFLWYVKQCGGTTRIFSVTNGGQERKF 219

Qy 264 -GGSDLLPEAFLSVLDVPILLNSKVKHIRQSDKGVIVSYQTGNESSLMDLSADIVLVTTT 322

Db 220 VGGSGQVSERIMDLLGDQVKLNHPVTHVDQSSDNIIIE-TLNHEHYECKYVINNIPPTLT 278

Qy 323 AKAALFIDFDPPLSISKWEALRSVHYDSSTKILLTFRDKFWEDDGIRGGKSITDGPSRYI 382

Db 279 AK---IHFRPELPAENGLIGRLPMGAVIKCMMYKEAFWKKDYGCMIIEDEDAFL 333

Qy 383 YYPSHFHTNET------IGVLLASYTWSDESLLFLGASDELKELALRDL-AKIHG 432

Db 334 -----SITLDDTKPDGSLPAIMGFILARK-ADR----LAKLHKEIRKKICELYAKVLG 382

Qy 433 EQVWDKCTGVIVKKWSADPYSLGAF-ALFTPYQHLEYAQELFSSEGRVHFAGEHTA---- 487

Db 383 SQEALHPVHYEEKNWCEEQYSGGCYTAYFPPGIMTQYGRVIRQPVGRIFFFAGTETATKWS 442

Qy 488 -FPHAMIETSMKSAIRAATNINKVANEESTIEHTKDE 523

Db 443 GYMEGAVEAGERAAREVLNGLGKVTEKDIWVQEFESK 479
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warch completed: October 4, 2005, 14:04:27